

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 12/23
Searcher: P. Schreiber - 308-4792
Terminal time: 3 7
Elapsed time: 17
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
☒ CM-1 6403
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Type of Search
____ N.A. Sequence
10 A.A. Sequence
____ Structure
____ Bibliographic

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____ IG
____ STN
____ Dialog
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____ DARC/Questel
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 9.12597 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-2

Perfect score: 101

Sequence: 1 WIDPENGDSGYAPRFQG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	17	AA197230	Complementary dete
2	101	100.0	17	AAU74407	Heavy chain comple
3	101	100.0	117	AA197235	Variable heavy cha
4	101	100.0	117	AAU74412	Antigen-binding pr
5	101	100.0	240	AAU74419	Antigen-binding pr
6	94	93.1	17	AAE13138	Humanised antibody
7	94	93.1	17	AA197204	VEGF antagonist an
8	94	93.1	17	AAU74416	Heavy chain comple
9	94	93.1	117	AAE13143	Humanised antibody
10	94	93.1	117	AA1982709	VEGF antagonist an

11	94	93.1	117	23	AAU74417	Antigen-binding pr
12	94	93.1	136	22	AAE13145	Chimeric pIC11 hea
13	94	93.1	136	22	AAE13145	VEGF antagonist an
14	94	93.1	238	23	AAU74420	Antigen-binding pr
15	90	89.1	17	20	AAW89162	Anti-p53 monoclonal
16	90	89.1	20	21	AAU70794	Murine anti-p53 PA
17	90	89.1	112	20	AAW89173	Anti-p53 monoclonal
18	90	89.1	116	21	AAU70787	Murine anti-p53 mo
19	90	89.1	122	20	AAU39531	Humanised Murine C
20	90	89.1	124	15	AAW60565	Anti-carcinomaembryo
21	90	89.1	124	15	AAW60566	Anti-carcinomaembryo
22	90	89.1	124	20	AAU39528	Murine COL1 VH cha
23	90	89.1	124	20	AAU39530	Humanised Murine C
24	90	89.1	124	20	AAU39536	Humanised Murine C
25	90	89.1	124	20	AAU39537	Humanised Murine C
26	90	89.1	124	20	AAU39538	Humanised Murine C
27	90	89.1	124	20	AAU39539	Humanised Murine C
28	90	89.1	124	20	AAU39540	Humanised Murine C
29	90	89.1	124	20	AAU39541	Humanised Murine C
30	90	89.1	124	20	AAU39542	Humanised Murine C
31	90	89.1	124	20	AAU39543	Humanised Murine C
32	90	89.1	124	23	AAU76632	Murine Col-1(CEA a
33	90	89.1	124	23	AAU76634	Humanised COL-1(CE
34	90	89.1	124	23	AAU76635	Humanised COL-1(CE
35	90	89.1	124	23	AAU76636	Humanised COL-1(CE
36	90	89.1	124	23	AAU76637	Humanised COL-1(CE
37	90	89.1	124	23	AAU76638	Humanised COL-1(CE
38	90	89.1	124	23	AAU76639	Humanised COL-1(CE
39	90	89.1	124	23	AAU76640	Humanised COL-1(CE
40	90	89.1	124	23	AAU76641	Humanised COL-1(CE
41	90	89.1	124	23	AAU76642	Humanised COL-1(CE
42	90	89.1	124	23	AAU76643	Humanised COL-1(CE
43	90	89.1	124	23	AAU76650	Protein template u
44	90	89.1	243	19	AAW60769	Single chain antib
45	90	89.1	270	16	AAU75719	MFE-23 antibody.

ALIGNMENTS

RESULT 1
AA197230
ID AA197230 standard; Protein; 17 AA.
XX
AC AA197230;
XX
DT 19-DEC-2000 (first entry)
XX
DE Complementary determining region (CDRH2) of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US02180.
XX
PR 29-JAN-1999; 99US-0117726.
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z, Witte L;

XX WPI; 2000-505966/45.
DR N-PSDB; AA53762.
XX
PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
XX used to reduce tumour growth
XX
XX Claim 3; Page 50; 55pp; English.
PS
XX New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementarity determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 101; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSGYAPKFG 17
| | | | | | | | | | | | | | | | |
Db 1 WIDPENGSGYAPKFG 17
| | | | | | | | | | | | | | | | |
RESULT 2
AAU74407
ID AAU74407; standard; peptide; 17 AA.
XX
XX AAU74407;
AC
XX
DT 26-MAR-2002 (first entry)
XX
DE Heavy chain complementarity determining region H2 (CDRH2) version #1.
XX
XX Complementarity determining region; CDR; CDRH2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody; heavy chain variable domain.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
XX
XX 24-MAY-2000; 2000US-206749P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2002-106189/14.
DR N-PSDB; AAS20278.
XX
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX

PS
XX Claim 55; Page 56; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the FC region (e.g., CH2 and CH3 for an Ig molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the heavy chain variable domain
CC complementarity determining region H2 (CDRH2) version #1 incorporated
CC into an antigen-binding protein described in the method of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 101; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSGYAPKFG 17
| | | | | | | | | | | | | | | | |
Db 1 WIDPENGSGYAPKFG 17
| | | | | | | | | | | | | | | | |
RESULT 3
AAU97235
ID AAU97235 standard; Protein; 117 AA.
XX
XX AAU97235;
AC
XX
DT 19-DEC-2000 (first entry)
XX
DE Variable heavy chain fragment of anti-SI(KDR) antibody.
XX
XX Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200044777-A1.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US02180.
XX
XX 29-JAN-1999; 99US-0117726.
PR
XX 29-JAN-1999; 99US-0240736.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z, Witte L;
PI
XX WPI; 2000-505966/45.
DR N-PSDB; AA53767.
XX

PT Novel immunoglobulin molecules binding kinase insert domain-containing
 PT receptor with the same affinity as vascular endothelial growth factor,
 PT used to reduce tumour growth

PS Claim 4; Page 50-51; 55pp; English.

XX New immunoglobulin molecules are described that bind kinase insert
 CC domain-containing receptor (KDR) with a comparable affinity to human
 CC vascular endothelial growth factor (VEGF). The antibodies neutralise
 CC KDR activation. The immunoglobulin may be a multivalent single
 CC chain antibody, a monovalent single chain antibody, a diabody, a
 CC triabody, a humanised antibody or a chimerised antibody.

CC The immunoglobulin molecules bind specifically to an
 CC extracellular domain of the KDR receptor with the same affinity as
 CC VEGF. Overexpression of VEGF has been implicated in a number of
 CC human tumour cell lines including glioblastoma multiforme,
 CC hemangioblastoma, central nervous system neoplasms and AIDS
 CC associated Kaposi's sarcoma. The antibodies therefore have
 CC applications in treating these conditions. This sequence encodes a
 CC preferred heavy chain complementary determining region of the
 CC immunoglobulins of the invention.

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.7e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSGYAPKFGQ 17
 | | | | | | | | | | | | | | | | | | | |
 Db 50 WIDPENGSGYAPKFGQ 66

RESULT 4

AAU74412
 ID AAU74412 standard; peptide; 117 AA.

XX AC AAU74412;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein heavy chain variable domain (VH) #1.

XX KW Antigen-binding protein; antibody heavy chain variable domain;
 KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 KW cell proliferation inhibitor.

XX OS Mus sp.

XX PN WO200190192-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX DR WPI; 2002-106189/14.

XX DR N-PSDB; AAS20283.

XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides

XX PS Claim 57; Page 57; 64pp; English.

XX CC The invention describes an antigen-binding protein (P1) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This sequence represents a heavy chain variable domain (VH) incorporated
 CC into Fv, an engineered protein containing a heavy chain variable domain
 CC and a light chain variable domain in one polypeptide chain, described in
 CC the method of the invention.

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.7e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSGYAPKFGQ 17
 | | | | | | | | | | | | | | | | | | | |
 Db 50 WIDPENGSGYAPKFGQ 66

RESULT 5

AAU74419
 ID AAU74419 standard; Protein; 240 AA.

XX AC AAU74419;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein, single chain variable fragment version #1.

XX KW Antigen-binding protein; single chain variable fragment; scFv; antigen;
 KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 KW cell proliferation inhibitor.

XX OS Mus sp.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT 1..117 /label= VH

XX FT /note= "Heavy chain variable domain. Specifically
 claimed in claim 57"

XX FT 118..132 /label= Linker

XX FT /note= "15 amino acid linker joins the VH and VL
 regions of the single chain variable
 fragment protein. Encoded by AAS20285"

XX FT 133..240 /label= VL

XX FT /note= "Light chain variable domain. Specifically
 claimed in claim 57"

XX FT WO200190192-A2.

XX PN 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.


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PI Kerbel R;
XX WPI; 2001-514531/56.
XX Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent
XX Disclosure; Page 37; 42pp; English.
XX The present sequence is that of complementarity determining region
CC 2 of the heavy chain variable region (see also AAB82701) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX Sequence 17 AA;

Query Match 93.1%; Score 94; DB 22; Length 17;
Best Local Similarity 94.1%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 1 WIDPENGDSGYAPKFG 17

RESULT 8
AAU74416
ID AAU74416 standard; peptide; 17 AA.
XX
AC AAU74416;
XX
DT 26-MAR-2002 (first entry)
XX
DE Heavy chain complementarity determining region H2 (CDRH2) version #2.
XX
DE Complementarity determining region; CDR; CDRH2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody heavy chain variable domain.
XX
OS SMus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
XX
XX 24-MAY-2000; 2000US-206749P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
PI WPI; 2002-106189/14.
XX
XX

DR N-PSDB; AAS20287.
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX Claim 59; Page 60; 64pp; English.
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an Ig molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the heavy chain variable domain
CC complementarity determining region H2 (CDRH2) version #2 incorporated
CC into an antigen-binding protein described in the method of the invention.
XX Sequence 17 AA;

Query Match 93.1%; Score 94; DB 23; Length 17;
Best Local Similarity 94.1%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 1 WIDPENGDSGYAPKFG 17

RESULT 9
AAE13143
ID AAE13143 standard; Protein; 117 AA.
XX
AC AAE13143;
XX
DT 28-JAN-2002 (first entry)
XX
DE Humanised antibody heavy chain fragment.
XX
DE Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10504.
XX
XX 31-MAR-2000; 2000US-0540770.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Witte L, Rafii S;
XX

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DR WPI; 2001-662942/76.
 XX N-PSDB; AAD21669.
 XX
 PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with
 PT an antagonist of a vascular endothelial growth factor receptor -
 XX
 PS Claim 8; Page 15; 68pp; English.
 XX
 CC The invention relates to a method for inhibiting the growth of non-solid
 CC tumour cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to
 CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
 CC antibody heavy chain fragment used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 117 AA;
 Query Match 93.1%; Score 94; DB 22; Length 117;
 Best Local Similarity 94.1%; Pred. No. 8e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 WIDPENGSGYAPKFGQ 17
 Db WIDPENGSGYAPKFGQ 66
 WIDPENGSGYAPKFGQ 66
 WIDPENGSGYAPKFGQ 66
 RESULT 10
 AAB82709
 ID AAB82709 standard; Protein; 117 AA.
 XX
 AC AAB82709;
 XX
 DT 15-OCT-2001 (first entry)
 DE
 DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.
 XX
 XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
 KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
 KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
 KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
 KW colon carcinoma; ovarian carcinoma; neuroblastoma;
 KW glioblastoma multiforme; melanoma; therapy; heavy chain.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 26..35
 FT /label= CDR-H1
 FT /note= "complementarity determining region 1"
 FT Region 50..66
 FT /label= CDR-H2
 FT /note= "complementarity determining region 2"
 FT Region 99..106
 FT /label= CDR-H3
 FT /note= "complementarity determining region 3"
 XX
 PN WO200154723-A1.
 XX
 PD 02-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US02839.
 XX
 XX 28-JAN-2000; 2000US-0178791.

PR 31-MAR-2000; 2000US-0539692.
 XX
 PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Kerbel R;
 XX
 XX WPI; 2001-514531/56.
 DR N-PSDB; AAH26405.
 XX
 XX Treating or controlling an angiogenic dependent condition (e.g. a
 PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
 PT administering a combination of an antiangiogenic molecule and a
 PT chemotherapeutic agent -
 XX
 PS Disclosure; Page 38; 42pp; English.
 XX
 CC The present sequence is that of the heavy chain variable region of
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,
 CC or a fragment of it, can be used as an anti-angiogenic molecule,
 CC together with a chemotherapeutic acid, for the treatment of an
 CC angiogenic dependent condition in a mammal, especially a human.
 CC The invention relates generally to a method of treating or
 CC controlling an angiogenic dependent condition by administering an
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
 CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The anti-angiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include,
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
 XX
 SQ Sequence 117 AA;
 Query Match 93.1%; Score 94; DB 22; Length 117;
 Best Local Similarity 94.1%; Pred. No. 8e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 WIDPENGSGYAPKFGQ 17
 Db WIDPENGSGYAPKFGQ 66
 WIDPENGSGYAPKFGQ 66
 WIDPENGSGYAPKFGQ 66
 RESULT 11
 AAU74417
 ID AAU74417 standard; peptide; 117 AA.
 XX
 AC AAU74417;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Antigen-binding protein heavy chain variable domain (VH) #2.
 DE
 XX Antigen-binding protein; antibody heavy chain variable domain;
 KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 XX cell proliferation inhibitor.
 OS Mus sp.
 XX
 PN WO200190192-A2.
 XX
 PD 29-NOV-2001.
 XX
 XX 24-MAY-2001; 2001WO-US16924.
 PF
 XX 24-MAY-2000; 2000US-206749P.
 PR
 XX

PA (IMCL-) IMCLONE SYSTEMS INC.
 XX Zhu Z;
 XX
 XX WPI; 2002-106189/14.
 DR N-PSDB; AAS20288.
 XX
 XX New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides
 XX
 XX Claim 61; Page 60; 64pp; English.
 PS
 XX The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This sequence represents a heavy chain variable domain (VH) incorporated
 CC into Fv; an engineered protein containing a heavy chain variable domain
 CC and a light chain variable domain in one polypeptide chain, described in
 CC the method of the invention.
 XX
 XX SQ Sequence 117 AA;
 Query Match 93.1%; Score 94; DB 23; Length 117;
 Best Local Similarity 94.1%; Pred. No. 8e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 WIDPENGSDGYAPKFG 17
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 Db 50 WIDPENGSDGYAPKFG 66
 RESULT 12
 ID AAE13145 standard; Protein; 136 AA.
 XX AAE13145;
 XX
 XX 28-JAN-2002 (first entry)
 XX
 XX Chimeric pIC11 heavy chain fragment.
 XX
 XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
 KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
 KW human; pIC11 vector.
 XX
 XX Chimeric - Homo sapiens.
 OS Chimeric - Unidentified.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Leader_peptide
 FT Protein 20..136
 FT /note= "Mature chimeric pIC11 heavy chain fragment"
 FT Region 45..54
 FT /label= CDR_H1

FT Region 69..85
 FT /label= CDR_H2
 FT Misc-difference 84
 FT /note= "Residue 'O' is present at this location in the
 FT sequence shown in fig-11 of the specification"
 FT Misc-difference 101
 FT /note= "Residue 'O' is present at this location in the
 FT sequence shown in fig-11 of the specification"
 FT Region 119..125
 FT /label= CDR_H3
 XX
 XX WO200174296-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10504.
 XX
 XX 31-MAR-2000; 2000US-0540770.
 XX
 XX (IMCL-) IMCLONE SYSTEMS INC.
 XX (CORR) CORNELL RES FOUND INC.
 XX Witte L, Rafil S;
 XX
 XX WPI; 2001-662942/76.
 XX N-PSDB; AAD21682.
 XX
 XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with
 PT an antagonist of a vascular endothelial growth factor receptor -
 XX
 XX Example 3; Fig 11; 68pp; English.
 XX
 XX The invention relates to a method for inhibiting the growth of non-solid
 CC tumour cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to
 CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
 CC pIC11 heavy chain fragment which is used for the construction of chimeric
 CC pIC11 IgG expression vector. Chimeric pIC11 heavy chain contains cloned
 CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
 CC domain (CH).
 XX
 XX SQ Sequence 136 AA;
 Query Match 93.1%; Score 94; DB 22; Length 136;
 Best Local Similarity 94.1%; Pred. No. 9.4e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 WIDPENGSDGYAPKFG 17
 ||||| |||||
 Db 69 WIDPENGSDGYAPKFG 85
 RESULT 13
 ID AAB82701 standard; Protein; 136 AA.
 XX AAB82701;
 XX
 XX 15-OCT-2001 (first entry)
 XX
 XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.
 DE IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
 KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
 KW

CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This is the amino acid sequence of a single chain variable fragment
 CC (scfv), an engineered protein containing a variable light and variable
 CC heavy domain on one polypeptide, described in the method of the
 CC invention.

XX SQ Sequence 238 AA;

Query Match 93.1%; Score 94; DB 23; Length 238;

Best Local Similarity 94.1%; Pred. No. 1.7e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WIDPENGDSGYAPKFOG 17

Db 50 WIDPENGDSGYAPKFOG 66

RESULT 15

AAW89162

ID AAW89162 standard; peptide; 17 AA.

XX AC

XX AAW89162;

XX DT 25-MAR-1999 (first entry)

XX DE Anti-p53 monoclonal antibody 421 CDR2 heavy chain based peptide.

XX EE Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;

XX KW immune response; tumour associated antigen; metastatic cancer.

XX OS Mus sp.

XX OS Synthetic.

XX FN WO9856416-A1.

XX PD 17-DEC-1998.

XX XX 09-JUN-1998; 98WO-IL00266.

XX XX 09-JUN-1997; 97IL-0121041.

XX PR (YEDA) YEDA RES & DEV CO LTD.

XX PA

XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;

XX PI Wolkowicz R;

XX DR WPI; 1999-070296/06.

XX XX

XX PT Use of a monoclonal antibody to a tumour-associated antigen - to

XX PT induce anti-tumour immunity or elicit an increased immune response

XX PT to the antigen

XX XX

XX PS Claim 7; Page 29; 47pp; English.

XX CC

XX CC The present invention describes the use of an immunogen (A) to induce

XX CC anti-tumour immunity; to elicit an increased immune response to tumour

XX CC associated antigen (TAA) and/or to induce an immune response to mutant

XX CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody

XX CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR

XX CC (complementarity determining region) on the heavy or light chain of Mab

XX CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the

XX CC variable (V) region of Mab, in a gene delivery vehicle. The present

XX CC sequence represents a peptide based on CDR2 of the heavy chain of

XX CC anti-p53 Mab 421. Also described is a method for generating sequence-

XX CC specific, anti-DNA antibodies (Ab) by immunising a mammal with a Mab

XX CC directed to a domain containing a DNA-binding site of a DNA-binding

XX CC protein. (A) is used to treat a wide variety of primary and metastatic

XX CC cancers, particularly those where p53 is involved. Ab are used for

XX CC diagnosis (e.g to determine critical sequences in animal or plant

XX CC breeding); to identify bacteria and other parasites; to determine

CC parentage; in forensic science; to isolate specific genes for DNA
 CC vaccination; in gene sequencing and cloning; also possibly for activation
 CC of selected therapeutic genes in plants, animals and humans. (A) induce
 CC an effective anti-tumour response without causing harm to the patient.
 CC The method uses (A) to generate anti-TAA by exploiting the anti-idiotypic
 CC network.

XX SQ Sequence 17 AA;

Query Match 89.1%; Score 90; DB 20; Length 17;

Best Local Similarity 88.2%; Pred. No. 4.3e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WIDPENGDSGYAPKFOG 17

Db 1 WIDPENGDTYAPKFOG 17

Search completed: December 23, 2002, 07:25:03

Job time : 10.126 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 3.06395 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-2

Perfect score: 101

Sequence: 1 WIDPENGDSGVAPKFGQ 17

Scoring table: BLOSUM62

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	90	89.1	124	1	US-08-017-570-6
3	90	89.1	124	1	US-08-471-426-4
4	90	89.1	124	1	US-08-471-426-6
5	90	89.1	124	4	US-09-672-609-1
6	90	89.1	124	4	US-09-672-609-3
7	90	89.1	124	4	US-09-672-609-4
8	90	89.1	124	4	US-09-672-609-5
9	90	89.1	124	4	US-09-672-609-6
10	90	89.1	124	4	US-09-672-609-7
11	90	89.1	124	4	US-09-672-609-8
12	90	89.1	124	4	US-09-672-609-9
13	90	89.1	124	4	US-09-672-609-10
14	90	89.1	124	4	US-09-672-609-11
15	90	89.1	124	4	US-09-672-609-12
16	90	89.1	124	4	US-09-025-403A-1
17	90	89.1	124	4	US-09-025-403A-3
18	90	89.1	124	4	US-09-025-403A-4
19	90	89.1	124	4	US-09-025-403A-5
20	90	89.1	124	4	US-09-025-403A-6
21	90	89.1	124	4	US-09-025-403A-7
22	90	89.1	124	4	US-09-025-403A-8
23	90	89.1	124	4	US-09-025-403A-9
24	90	89.1	124	4	US-09-025-403A-10
25	90	89.1	124	4	US-09-025-403A-11
26	90	89.1	124	4	US-09-025-403A-12
27	90	89.1	124	5	PCT-US94-01709-4

28	90	89.1	124	5	PCT-US94-01709-6
29	90	89.1	270	2	US-08-652-507-2
30	90	89.1	535	4	US-08-983-035A-38
31	90	89.1	553	2	US-08-661-052-16
32	90	89.1	553	4	US-09-188-082-16
33	90	89.1	553	4	US-09-364-088-16
34	90	89.1	553	4	US-09-102-716-16
35	86	85.1	17	4	US-09-171-945-31
36	86	85.1	120	4	US-09-171-945-11
37	86	85.1	120	4	US-09-171-945-55
38	86	85.1	120	4	US-09-171-945-75
39	86	85.1	120	4	US-09-171-945-79
40	86	85.1	120	4	US-09-171-945-81
41	86	85.1	120	4	US-09-171-945-85
42	86	85.1	120	4	US-09-171-945-89
43	86	85.1	120	4	US-09-171-945-91
44	86	85.1	255	4	US-09-171-945-19
45	86	85.1	255	4	US-09-171-945-57

ALIGNMENTS

RESULT 1
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLON, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-017-570-4

Query Match 89.1%; Score 90; DB 1; Length 124;

Best Local Similarity 88.2%; Pred. No. 4e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGVAPKFGQ 17

|||||||: |||||

Db 50 WIDPENGDTYAPKFGQ 66

RESULT 2
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; Sequence 6, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-6
Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66
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US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US

ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4
Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDTYAPKFG 66
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US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6
Query Match 89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

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Query Match      89.1%; Score 90; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels
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RESULT 5
US-09-672-609-1
; Sequence 1, Application US/09672609

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Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels
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RESULT 6
US-09-672-609-3
; Sequence 3, Application US/09672609

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: LENGTH: 124
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Humanized COL-1 VH, HuVH
: LOCATION: 1..124
: OTHER INFORMATION: Humanized heavy chain variable region containing human
: OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRs, and Phe-27, Asn-28,
: OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
: US-09-672-609-3

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Query Match	89.1%	Score 90;	DB 4;	Length 124;
Best Local Similarity	88.2%	Pred. No. 4e-07;		
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; Sequence 4, Application US/09672609

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Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels

RESULT 8
US-09-672-609-5
; Sequence 5, Application US/09672609

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: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/672,609
: CURRENT FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 09/025,403
: PRIOR FILING DATE: 1998-02-18
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Microsoft Word 97 SR-2
: SEQ ID NO 3
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; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHAT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-672-609-5

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDEYAPKFG 66

RESULT 9
US-09-672-609-6
; Sequence 6, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 6
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHAA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
US-09-672-609-6

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDEYAPKFG 66

RESULT 10
US-09-672-609-7
; Sequence 7, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.

; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
US-09-672-609-7

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDEYAPKFG 66

RESULT 11
US-09-672-609-8
; Sequence 8, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 8
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHATAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
Db 50 WIDPENGDEYAPKFG 66

RESULT 12
US-09-672-609-9
; Sequence 9, Application US/09672609
; Patent No. 6333405

GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 9
LENGTH: 124
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHSTAY
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
OTHER INFORMATION: Thr-98
US-09-672-609-9

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSGYAPKFGQ 17
|||||||: |||||
Db 50 WIDPENGDTYAPKFGQ 66

RESULT 13
US-09-672-609-10
Sequence 10, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 10
LENGTH: 124
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHT
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
US-09-672-609-10

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSGYAPKFGQ 17
|||||||: |||||
Db 50 WIDPENGDTYAPKFGQ 66

RESULT 14
US-09-672-609-11
Sequence 11, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 11
LENGTH: 124
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHS
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
US-09-672-609-11

Query Match 89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSGYAPKFGQ 17
|||||||: |||||
Db 50 WIDPENGDTYAPKFGQ 66

RESULT 15
US-09-672-609-12
Sequence 12, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 12
LENGTH: 124
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHSTAY
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC
OTHER INFORMATION: CEL-12208, and containing human NEWM VH FRs, murine COL-1 VH C
OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL-1 VH C
OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79,
OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
US-09-672-609-12

Query Match 89.1%; Score 90; DB 4; Length 124;

Best Local Similarity 88.2%; Pred. No. 4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels

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QY 1 WIDPENGDSGYAPKFG 17
      |||||: |||||
Db 50 WIDPENGDEYAPKFG 66
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Search completed: December 23, 2002, 07:33:12
Job time : 4.06395 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 1.5814 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-2

Perfect score: 101

Sequence: 1 WIDPENGDSGYAPKFGQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	101	100.0	17	10	US-09-865-198-2
3	101	100.0	117	10	US-09-976-787-7
4	101	100.0	117	10	US-09-865-198-7
5	101	100.0	240	10	US-09-976-787-28
6	101	100.0	240	10	US-09-865-198-27
7	94	93.1	17	10	US-09-976-787-22
8	94	93.1	17	10	US-09-865-198-21
9	94	93.1	117	10	US-09-976-787-23
10	94	93.1	117	10	US-09-865-198-22
11	94	93.1	238	10	US-09-976-787-29
12	94	93.1	238	10	US-09-865-198-28
13	90	89.1	124	9	US-09-974-052-1
14	90	89.1	124	9	US-09-974-052-3
15	90	89.1	124	9	US-09-974-052-4
16	90	89.1	124	9	US-09-974-052-5
17	90	89.1	124	9	US-09-974-052-6
18	90	89.1	124	9	US-09-974-052-7
19	90	89.1	124	9	US-09-974-052-8

20	89.1	124	9	US-09-974-052-9	Sequence 9, Appli
21	89.1	124	9	US-09-974-052-10	Sequence 10, Appli
22	89.1	124	9	US-09-974-052-11	Sequence 11, Appli
23	89.1	124	9	US-09-974-052-12	Sequence 12, Appli
24	89.1	124	9	US-09-974-051-1	Sequence 1, Appli
25	89.1	124	9	US-09-974-051-3	Sequence 3, Appli
26	89.1	124	9	US-09-974-051-4	Sequence 4, Appli
27	89.1	124	9	US-09-974-051-5	Sequence 5, Appli
28	89.1	124	9	US-09-974-051-6	Sequence 6, Appli
29	89.1	124	9	US-09-974-051-7	Sequence 7, Appli
30	89.1	124	9	US-09-974-051-8	Sequence 8, Appli
31	89.1	124	9	US-09-974-051-9	Sequence 9, Appli
32	89.1	124	9	US-09-974-051-10	Sequence 10, Appli
33	89.1	124	9	US-09-974-051-11	Sequence 11, Appli
34	89.1	124	9	US-09-974-051-12	Sequence 12, Appli
35	85.1	17	10	US-09-910-059-31	Sequence 31, Appli
36	85.1	120	10	US-09-910-059-11	Sequence 11, Appli
37	85.1	120	10	US-09-910-059-55	Sequence 55, Appli
38	85.1	120	10	US-09-910-059-75	Sequence 75, Appli
39	85.1	120	10	US-09-910-059-79	Sequence 79, Appli
40	85.1	120	10	US-09-910-059-81	Sequence 81, Appli
41	85.1	120	10	US-09-910-059-85	Sequence 85, Appli
42	85.1	120	10	US-09-910-059-89	Sequence 89, Appli
43	85.1	120	10	US-09-910-059-91	Sequence 91, Appli
44	85.1	255	10	US-09-910-059-19	Sequence 19, Appli
45	85.1	255	10	US-09-910-059-57	Sequence 57, Appli

ALIGNMENTS

RESULT 1

US-09-976-787-2

; Sequence 2, Application US/09976787

; Patent No. US20020064528A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; APPLICANT: Witte, Larry

; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

; FILE REFERENCE: 11245/46505

; CURRENT APPLICATION NUMBER: US/09/976,787

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/493,539

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 2

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Mus musculus

; US-09-976-787-2

Query Match	100.0%;	Score 101;	DB 10;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 1.5e-09;		
Matches	17;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy 1 WIDPENGDSGYAPKFGQ 17

Db 1 WIDPENGDSGYAPKFGQ 17

RESULT 2

US-09-865-198-2

; Sequence 2, Application US/09865198

; Patent No. US20020103345A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me

; TITLE OF INVENTION: Production

; FILE REFERENCE: 11245/47102

; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2

Query Match 100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||
Db 1 WIDPENGDSGYAPKFOG 17

RESULT 3

US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 4

US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 5

US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 101; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 6

US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 101; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 7

US-09-976-787-22


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; Sequence 22, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-22

Query Match          93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
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Db 1 WIDPENGDSYAPKFG 17

RESULT 8
US-09-865-198-21
; Sequence 21, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-21

Query Match          93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
   ||||| ||||| |||||
Db 1 WIDPENGDSYAPKFG 17

RESULT 9
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
```

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; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match          93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
   ||||| ||||| |||||
Db 50 WIDPENGDSYAPKFG 66

RESULT 10
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match          93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
   ||||| ||||| |||||
Db 50 WIDPENGDSYAPKFG 66

RESULT 11
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match          93.1%; Score 94; DB 10; Length 238;
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Best Local Similarity 94.1%; Pred. No. 2.6e-07; Mismatches 0; Indels 1; Gaps 0;
Matches 16; Conservative 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 12

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 93.1%; Score 94; DB 10; Length 238;

Best Local Similarity 94.1%; Pred. No. 2.6e-07; Mismatches 0; Indels 1; Gaps 0;
Matches 16; Conservative 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 13

US-09-974-052-4
; Sequence 1, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-052-4

Query Match 89.1%; Score 90; DB 9; Length 124;

Best Local Similarity 88.2%; Pred. No. 5.4e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1;

Query Match 89.1%; Score 90; DB 9; Length 124;

Best Local Similarity 88.2%; Pred. No. 5.4e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1;

QY 1 WIDPENGDSGYAPKFOG 17
|||||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 14

US-09-974-052-3
; Sequence 3, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-3

Query Match 89.1%; Score 90; DB 9; Length 124;

Best Local Similarity 88.2%; Pred. No. 5.4e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1;

QY 1 WIDPENGDSGYAPKFOG 17
|||||||
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 15

US-09-974-052-4
; Sequence 4, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 4
; LENGTH: 124
; TYPE: PRT
US-09-974-052-4

Query Match 89.1%; Score 90; DB 9; Length 124;

Best Local Similarity 88.2%; Pred. No. 5.4e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1;

Query Match 89.1%; Score 90; DB 9; Length 124;

Best Local Similarity 88.2%; Pred. No. 5.4e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1;

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; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRS, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-4

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Query Match      89.1%; Score 90; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 WIDPENGSGYAPKFG 17
   |||||: |||||
Db 50 WIDPENGTEYAPKFG 66

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Search completed: December 23, 2002, 07:58:18
Job time : 2.5814 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 3.36047 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-2

Perfect score: 101

Sequence: 1 WIDPENGDSGYAPKFGQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	89.1	82	2	A36025
2	82	81.2	118	2	S25174
3	82	81.2	136	2	S04576
4	80	79.2	116	2	S15672
5	78	77.2	137	2	S24445
6	67	66.3	85	2	E37262
7	67	66.3	98	2	S26918
8	67	66.3	132	2	S31596
9	67	66.3	136	2	S31600
10	67	66.3	143	1	EJHUND
11	64	63.4	86	2	S54912
12	64	63.4	110	2	PH1670
13	64	63.4	171	2	S23623
14	63	62.4	127	2	S34014
15	62	61.4	98	2	S26938
16	62	61.4	98	2	S26912
17	62	61.4	99	2	D37262
18	62	61.4	107	2	PH1013
19	62	61.4	108	2	PH1012
20	62	61.4	117	2	S31680
21	62	61.4	117	2	S31551
22	62	61.4	118	2	S36265
23	62	61.4	120	2	S03471
24	62	61.4	122	2	S06823
25	62	61.4	123	2	D33548
26	62	61.4	123	2	PH1403
27	62	61.4	129	2	S46393
28	62	61.4	135	2	S49530
29	60	59.4	120	2	S03484

ALIGNMENTS

RESULT 1

A36025

Ig heavy chain V region (PR8-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999

C:Accession: A36025; E36025

R:Caton, A.J.; Koprowski, H.

Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990

A:Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinator
A:Reference number: A36025; MUID:90349634; PMID:1696733

A:Accession: A36025

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-82 <CAZ>

A:Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956

A:Note: PR8-1

A:Accession: E36025

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 19-82 <CAZ>

A:Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964

A:Note: clone PR8-21

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 90; DB 2; Length 82;
Best Local Similarity 88.2%; Pred. No. 4.4e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WIDPENGDSGYAPKFGQ 17

|||||

Db 12 WIDPENGDTETAPKFGQ 28

RESULT 2

S25174

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S25174; S33133

R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.

submitted to the EMBL Data Library, July 1992

A:Description: Structure and binding properties of monoclonal antibodies to core hist
A:Reference number: S25174

A:Accession: S25174

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MON>

A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259

A:Accession: S33133

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MO2>
A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||1111: || |||||
Db 50 WIDPENGDTQYASKFOG 66

RESULT 3

S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04576

R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: involve
A:Reference number: S04573; MUID:87133856; PMID:3102255

A:Accession: S04576
A:Molecule type: mRNA
A:Residues: 1-136 <KOF>

A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 136;
Best Local Similarity 82.4%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||1111: || |||||
Db 69 WIDPENGDTQYASKFOG 85

RESULT 4

S15672
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S15672

R:Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,
Bio/Technology 9, 266-271, 1991
A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi
A:Reference number: S15672; MUID:91337412; PMID:1367535

A:Accession: S15672
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-116 <TEM>

A:Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979
C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 80; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 2.4e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||1111: || |||||
Db 50 WIDPENGDTQYASKFOG 66

RESULT 5

S2445
Ig heavy chain V region precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S2445

R:Berdoz, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged
A:Reference number: S2445

A:Accession: S2445
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-137 <BER>

A:Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:34-115/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 78; DB 2; Length 137;
Best Local Similarity 76.5%; Pred. No. 6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17
|||||1111: || |||||
Db 69 WIDPENGTVYDPKFOG 85

RESULT 6

E37262
Ig heavy chain V region (6H2) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-May-1997
C:Accession: E37262

R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: E37262
A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-85 <GOS>

A:Cross-references: GB:M57991
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 66.3%; Score 67; DB 2; Length 85;
Best Local Similarity 75.0%; Pred. No. 0.0019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFOG 17
|||||1111: || |||||
Db 29 IDPANGDTYDPKFOG 44

RESULT 7

S26918
Ig heavy chain V region (DP-15) - human (fragment)
C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:212317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0022;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
|:| |:| |:| |:| |:|
Db 50 WNPNSGNTGYAQRFG 66

RESULT 8

S31596
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31596

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <CUI>

A:Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 132;
Best Local Similarity 58.8%; Pred. No. 0.0031;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
|:| |:| |:| |:| |:|
Db 69 WNPNSGNTGYAQRFG 85

RESULT 9

S31600

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31600

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 136;
Best Local Similarity 58.8%; Pred. No. 0.0032;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
|:| |:| |:| |:| |:|
Db 69 WNPNSGNTGYAQRFG 85

RESULT 10

E1HUND

Ig heavy chain precursor V-I region (Nd) - human (fragments)

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000

C:Accession: A93933; A02026

R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: A93933
A:Molecule type: mRNA
A:Residues: 1-143 <KEN>

R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.

A:Reference number: A94418

A:Contents: annotation; partial sequence

A:Note: this epsilon chain was isolated from a myeloma protein

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>

F:30-113/Domain: immunoglobulin homology <IMM>

F:15/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi

F:37-111/Disulfide bonds: #status experimental

Query Match 66.3%; Score 67; DB 1; Length 143;
Best Local Similarity 58.8%; Pred. No. 0.0033;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
|:| |:| |:| |:| |:|
Db 65 WNPNSGNTYAPRFQ 81

RESULT 11

S54912

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C:Accession: S54912
R:Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G.
submitted to the EMBL Data Library, November 1992

A:Reference number: S54912

A:Accession: S54912

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <TOM>

A:Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:3-86/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 86;
Best Local Similarity 64.7%; Pred. No. 0.0057;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 17
|:| |:| |:| |:| |:|
Db 38 WNPNGSPSYAKKFG 54

RESULT 12

PH1670

Ig heavy chain V region (clone 2A12) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1670

R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staph

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1670

A:Molecule type: mRNA

A:Residues: 1-110 <HIL>

A:Experimental source: B cell

C; Species: Homo sapiens (man)

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EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; BE61CE63F8CE97BD CRC64;

Query Match 50.5%; Score 51; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.28;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IDPENGSGGYAPKFGG 17
DB 70 INPSGGSTSYAQKFCQG 85

RESULT 4
NUD9_HUMAN STANDARD; PRT; 350 AA.
AC Q9BW91;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)
DE (Adenosine diphosphate pyrophosphatase) (ADPP-Pase) (ADP-ribose phosphohydrolase) (Nucleoside diphosphate-linked moiety X motif 9).
GN NUDT9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=21279171; PubMed=11385575;
RA Perraud A.-L., Fleig A., Dunn C.A., Bagley L.A., Launay P., Schmitz C., Stokes A.J., Zhu Q., Bessman M.J., Penner R.; Kinet J.-P., Scharenberg A.M.;
RA "ADP-ribose gating of the calcium-permeable LTRPC2 channel revealed by Nudix motif homology."
RT Nature 411:595-599(2001).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ADP-ribose + H(2)O -> AMP + D-ribose 5-phosphate.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
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EMBL; AY026252; AAK07671.1; -.
DR EMBL; BC000542; AAH00542.1; -.
DR Genbank; HGNC:8056; NUDT9.

```
DR MTM; 606022; -.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00893; NUDIX; 1.
KW Hydrolase. 215 237 NUDIX BOX.
FT DOMAIN 215 237
SQ SEQUENCE 350 AA; 39125 MW; 2EA5B24B88FB3420 CRC64;

Query Match 49.5%; Score 50; DB 1; Length 350;
Best Local Similarity 46.7%; Pred. No. 1.4;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKF 15
| | | : | : | |
Db 110 WADPQISENPSKF 124

RESULT 5
HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IDPENGDSGYAPKFG 17
| : | | : | | : |
Db 51 INPNNGGTSYNQKPKG 66

RESULT 6
HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=800781170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IDPENGDSGYAPKFG 17
| : | | : | | : |
Db 51 INPNNGGTSYNQKPKG 66

RESULT 7
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IDPENGDSGYAPKFG 17
| : | | : | | : |
Db 51 INPNNGGTSYNQKPKG 66
```



```
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 AL/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 54 FRAMEWORK-2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 BY SIMILARITY.
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 850BC138856DFC9D CRC64;

Query Match 44.6%; Score 45; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 2.5;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGSGYAPKQFQ 17
Db 69 WYFGDGSTKYNERFKG 85

RESULT 11
VE4_HPV05
ID VE4_HPV05 STANDARD; PRT; 245 AA.
AC P06924;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable E4 protein.
OS Human papillomavirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10578;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87207670; PubMed=3033892;
RA Zachow K.R., Ostrow R.S., Faras A.J.;
RT "Nucleotide sequence and genome organization of human papillomavirus type 5.";
RL Virology 158:251-254(1987).
CC -----
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CC -----
DR EMBL; M17463; AAA46987.1; -.
DR PIR; E26277; W4WL5.
KW Early protein.
SQ SEQUENCE 245 AA; 25758 MW; 8F5ECDFB28D87E0 CRC64;

Query Match 44.6%; Score 45; DB 1; Length 245;
Best Local Similarity 61.5%; Pred. No. 5.7;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PENGSGGYAPKQFQ 16
Db 155 PHNGSHGHEPKVQ 167

RESULT 12
GLT1_WHEAT
ID GLT1_WHEAT STANDARD; PRT; 101 AA.
AC P02861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Glutenin, high molecular weight subunit PC256 (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Immunoglobulin V region; Signal.
OC SIGNAL 1 19
OC CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 AL/A4.
OC DOMAIN 20 49 FRAMEWORK-1.
OC DOMAIN 20 54 COMPLEMENTARITY-DETERMINING-1.
OC DOMAIN 55 54 FRAMEWORK-2.
OC DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.
OC DOMAIN 69 85 FRAMEWORK-3.
OC DOMAIN 86 117 BY SIMILARITY.
OC DISULFID 41 115
OC NON_TER 117 117
OC SEQUENCE 117 AA; 12971 MW; 850BC138856DFC9D CRC64;

Query Match 44.6%; Score 45; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 2.5;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGSGYAPKQFQ 17
Db 69 WYFGDGSTKYNERFKG 85

RESULT 13
GLN1_FRAAL
ID GLN1_FRAAL STANDARD; PRT; 474 AA.
AC P46033;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase I) (GSI).
DE (GSI).
DE GLNA.
OS Frankia alni.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Frankineae; Frankiaceae; Frankia.
OX NCBI_TaxID=1859;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cp11;
RX MEDLINE=93273742; PubMed=8099074;
RA Hosted T.J., Rochefort D.A., Benson D.R.;
RT "Close linkage of genes encoding glutamine synthetases I and II in Frankia alni Cp11."
RL J. Bacteriol. 175:3679-3684(1993).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate + L-glutamine.
CC -1- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO HEXAGONS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII) CAN BE FOUND IN THIS NITROGEN FIXING BACTERIA, GSI IS A TYPICAL
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CC PROKARYOTIC GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE
CC EUKARYOTIC ENZYME.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; L10631; ; NOT_ANNOTATED_CDS.
CC HSP; P06201; ILGR.
CC InterPro: IPR001691; GLN_synth.
CC InterPro: IPR004809; GlnA.
CC InterPro: IPR001637; GlnA_adenyln.
CC Pfam; PF00120; gln-synt; 1.
CC ProDom; PD001057; GlnA_adenyln; 1.
CC TIGRFAMS; TIGR00653; GlnA; 1.
CC PROSITE; PS00180; GLNA.1; 1.
CC PROSITE; PS00181; GLNA_ATP; 1.
CC PROSITE; PS00182; GLNA_ADENYLATION; 1.
CC Nitrogen fixation; Ligase; Multigene family.
CC BINDING 402 402 AMP (UNDER CONDITIONS OF ABUNDANT
CC FT GLUTAMINE) (BY SIMILARITY).
CC SEQUENCE 474 AA; 53951 MW; FE1DB19AC1735652 CRC64;
CC -----
CC Query Match 43.6%; Score 44; DB 1; Length 474;
CC Best Local Similarity 53.8%; Pred. No. 17;
CC Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
CC -----
CC 5 ENGDSGYAPKFG 17
CC 1 1 1 1 1 1 1
CC 168 EGGNMGYKPRFG 180
CC -----
CC RESULT 14
CC ROMA_KLEPN
CC ID ROMA_KLEPN STANDARD; PRT; 132 AA.
CC AC Q48412;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE Outer membrane protein roma (Fragment).
CC GN ROMA.
CC OS Klebsiella pneumoniae.
CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC OC Klebsiella.
CC OX NCBI_TaxID=573;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=66L8.
CC RX MEDLINE=96032015; PubMed=7551053;
CC RA George A.M., Hall R.M., Stokes H.W.;
CC RT "Multidrug resistance in Klebsiella pneumoniae: a novel gene, rama,
CC RT confers a multidrug resistance phenotype in Escherichia coli.";
CC RL Microbiology 141:1909-1920(1995).
CC CC -1- SIMILARITY: TO M.TUBERCULOSIS RV0906.
CC -----
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CC -----
CC EMBL; U79581; AAA85696.1; .
CC KW Outer membrane.
CC FT NON_TER 1 1
CC SEQUENCE 132 AA; 14745 MW; BCB216F27F9C853B CRC64;
CC -----
CC Query Match 42.6%; Score 43; DB 1; Length 132;
CC Best Local Similarity 63.6%; Pred. No. 6;
CC Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC 6 NGDSGYAPKFG 16
CC 1 1 1 1 1 1 1
CC 44 SGDSGYGPHFK 54
CC -----
CC RESULT 15
CC 17KD_RICPR
CC ID 17KD_RICPR STANDARD; PRT; 159 AA.
CC AC P16624;
CC DT 01-AUG-1990 (Rel. 15, Created)
CC DT 01-AUG-1991 (Rel. 19, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE 17 kDa surface antigen precursor.
CC GN OMP OR RP833.
CC OS Rickettsia prowazekii.
CC OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
CC OC Rickettsiaceae; Rickettsiae; Rickettsia.
CC OX NCBI_TaxID=782;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Madrid E;
CC RX MEDLINE=89359171; PubMed=2768201;
CC RA Anderson B.E., Tzianabos T.;
CC RT "Comparative sequence analysis of a genus-common rickettsial antigen
CC RT gene.";
CC RL J. Bacteriol. 171:5199-5201(1989).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Madrid E;
CC RX MEDLINE=99039499; PubMed=9823893;
CC RA Andersson S.G.E., Zomorodipour A., Andersson J.O., Naeslund A.K.,
CC RA Sierichitz-Ponten T., Alsmark U.C.M., Podowski R.M., Kurland C.G.;
CC RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
CC RT "The genome sequence of Rickettsia prowazekii and the origin of
CC RT mitochondria.";
CC RL Nature 396:133-140(1998).
CC CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC CC anchor (Probable).
CC -----
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CC -----
CC EMBL; M28482; AAA26378.1; ALT_SEQ.
CC DR EMBL; AJ235273; CAA15258.1; .
CC DR FIR; D33971; D33971.
CC DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC KW Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
CC FT SIGNAL 1 19
CC FT CHAIN 20 159 17 KDA SURFACE ANTIGEN.
CC FT LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
CC SQ SEQUENCE 159 AA; 16672 MW; A33D404B63EEB071 CRC64;
CC -----
CC Query Match 42.6%; Score 43; DB 1; Length 159;
CC Best Local Similarity 54.5%; Pred. No. 7.4;
CC Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC 1 WDPENGDSGY 11
CC 1 1 1 1 1 1 1
CC 102 WRNPNGNGHY 112
CC -----
CC Search completed: December 23, 2002, 07:26:02
CC Job time : 3.68023 secs
```

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 7.05039 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-2

Perfect score: 101

Sequence: 1 WIDPENGDSGYAPKFG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	75	74.3	468	11 Q99L31	Q99L31 mus musculus
2	58	57.4	614	4 Q96GA6	Q96GA6 homo sapien
3	57	56.4	109	11 Q99L85	Q99L85 mus musculus
4	56.5	55.9	150	4 Q9Y298	Q9Y298 homo sapien
5	56	55.4	497	4 Q8WY24	Q8WY24 homo sapien
6	55	54.5	125	4 Q9UL95	Q9UL95 homo sapien
7	54	53.5	119	4 Q9UL94	Q9UL94 homo sapien
8	54	53.5	481	11 Q8VCV5	Q8VCV5 mus musculus
9	51	50.5	124	4 Q9UL92	Q9UL92 homo sapien
10	50	49.5	300	11 Q9D0U2	Q9D0U2 mus musculus
11	50	49.5	350	4 Q96KB3	Q96KB3 homo sapien
12	50	49.5	500	4 Q9BRV0	Q9BRV0 homo sapien
13	49	48.5	754	10 Q94IL2	Q94IL2 secalc cere
14	49	48.5	754	10 Q94IK9	Q94IK9 secalc cere
15	49	48.5	754	10 Q93WF0	Q93WF0 secalc cere
16	48	47.5	311	16 Q92ME3	Q92ME3 rhizobium m

17 48 47.5 329 5 Q27501
18 48 47.5 403 16 Q8V1U7
19 48 47.5 484 11 Q99LA6
20 48 47.5 526 17 Q8TJE3
21 47.5 47.0 474 11 Q8R3H6
22 47 46.5 102 11 Q9JL79
23 47 46.5 208 16 Q92F12
24 47 46.5 209 16 Q8YA89
25 47 46.5 366 5 Q27528
26 47 46.5 375 5 Q9XW33
27 47 46.5 509 17 Q9HMH4
28 47 46.5 520 11 Q921T2
29 46 45.5 117 11 Q9QXF0
30 46 45.5 117 11 Q9QXE9
31 46 45.5 159 4 Q96GS0
32 46 45.5 327 5 Q23871
33 46 45.5 363 2 Q93NF9
34 46 45.5 390 9 Q9TIR0
35 46 45.5 481 11 Q91WT1
36 46 45.5 626 3 Q99112
37 45 45.5 1737 11 Q9J104
38 45.5 45.0 118 11 Q9Z1C4
39 45 44.6 138 2 Q9F8N0
40 45 44.6 168 17 Q27394
41 45 44.6 322 5 Q8SQW6
42 45 44.6 399 2 Q9KX26
43 45 44.6 405 16 Q98M10
44 45 44.6 638 16 Q92XY6
45 45 44.6 697 17 Q8TJQ4

ALIGNMENTS

RESULT 1

ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 74.3%; Score 75; DB 11; Length 468;

Best Local Similarity 75.0%; Pred. No. 0.0013;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGDSGYAPKFG 16

|||||:::|||||

Db 69 WIDPEDGETKYAPKFG 84

RESULT 2

Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6; (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Unknown (protein for MGC:15420).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-B-CELL;
RA Strausberg, K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -;
DR InterPro: IPR000005; HTHARAC.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 57.4%; Score 58; DB 4; Length 614;
Best Local Similarity 52.5%; Pred. No. 0.93;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFKQ 16
DB 69 WITPENGNTNYAQKFKQ 84

RESULT 3

Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Medline-20448942; PubMed-10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -;
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CE4ADE CRC64;

Query Match 56.4%; Score 57; DB 11; Length 109;
Best Local Similarity 58.8%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFKQ 17
DB 43 IDPATCHSKYDKPKFKQ 58

RESULT 4

Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE IgG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98322155; PubMed-9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monoclonal antibody derived from a hemophilia A patient with inhibitor";
RT Blood 92:496-506(1998).
RL EMBL; AJ224083; CAA11829.1; -;
DR HSSP; P01772; 2FBA.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 55.9%; Score 56.5; DB 4; Length 150;
Best Local Similarity 55.0%; Pred. No. 0.31;
Matches 11; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 WI---DPENGDSGYAPKFKQ 17
DB 66 WVGSDPESGESIYAREFQ 85

RESULT 5

Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SNC66, a Ig-like gene which is down-regulated in colorectal cancer";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -;
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 2.

RT fetus."

RN [1]

```

QY 1 WIDPENGDSGYAPKF 15
   | ||: :|:|||
Db 60 WADPQISENFSPKF 74

RESULT 11
Q96KB3 PRELIMINARY; PRT; 350 AA.
AC Q96KB3;
CT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE CDNA FLJ14389 fis, clone HEMBA1002876.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RC TISSUE=EMBRYO, AND MAINLY HEAD;
RA Isorai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RA "NEDO human cDNA sequencing project.";
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK027295; BAB55021.1;
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
SQ SEQUENCE 350 AA; 39042 MW; 8BE1A31ECCFB343D CRC64;

Query Match 49.5%; Score 50; DB 4; Length 350;
Best Local Similarity 46.7%; Pred. No. 8.9;
Matches 7; Conservative 4; Mismatches 4; Indels 0;

QY 1 WIDPENGDSGYAPKF 15
   | ||: :|:|||
Db 110 WADPQISENFSPKF 124

RESULT 12
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
CT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 54.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC005951; AAH05951.1;
DR HSP; P01789; IMCP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IIG_MHC; UNKNOWN_1.

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KW Hypothetical protein.
SQ SEQUENCE 500 AA: 54154 MW: 0A9BF43F2A3CC6D9 CRC64;
  Query Match      49.5%; Score 50; DB 4; Length 500;
  Best Local Similarity 47.1%; Pred. No. 14;
  Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17
  ||| : : : ||||
Db 69 WISPSDNTFRFAKFG 85

RESULT 13
Q94IL2 PRELIMINARY; PRT; 754 AA.
AC Q94IL2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
  encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
  orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314773; CAC40674.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA: 80179 MW: 89B4D795A3DC91BB CRC64;
  Query Match      48.5%; Score 49; DB 10; Length 754;
  Best Local Similarity 53.8%; Pred. No. 32;
  Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
  ||| | |||
Db 665 WLQPEQGQEGYYP 677

RESULT 14
Q94IK9 PRELIMINARY; PRT; 754 AA.
AC Q94IK9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
  encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
  orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314773; CAC40670.1; -.
DR EMBL; AJ314768; CAC40670.1; -.
DR EMBL; AJ314778; CAC40679.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 754 HMW GLUTENIN SUBUNIT X.
SQ SEQUENCE 754 AA: 80267 MW: 6F160E5F2545FC7 CRC64;
  Query Match      48.5%; Score 49; DB 10; Length 754;
  Best Local Similarity 53.8%; Pred. No. 32;
  Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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```
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
  encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SMITH;
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
  orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314779; CAC40680.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21 HMW GLUTENIN SUBUNIT X.
FT CHAIN 22 754
SQ SEQUENCE 754 AA: 80267 MW: 6F160E5F2545FC7 CRC64;
  Query Match      48.5%; Score 49; DB 10; Length 754;
  Best Local Similarity 53.8%; Pred. No. 32;
  Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
  ||| | |||
Db 665 WLQPEQGQEGYYP 677

RESULT 15
Q93WF0 PRELIMINARY; PRT; 754 AA.
AC Q93WF0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE High molecular weight glutenin subunit x precursor.
GN GLU-1R.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PETKUS;
RA de Bustos A., Jouve N.;
RT "Characterization and analysis of new subunits-like wheat HMW-glutenin
  encoded by Glu-1R gene of Secale cereale.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PETKUS;
RA de Bustos A., Rubio P., Jouve N.;
RT "Characterization of two gene subunits on the 1R chromosome of rye as
  orthologs of each of the Glu-1 genes of hexaploid wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ314768; CAC40670.1; -.
DR EMBL; AJ314778; CAC40679.1; -.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF03157; Glutenin_hmw; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 754 HMW GLUTENIN SUBUNIT X.
SQ SEQUENCE 754 AA: 80270 MW: 28A1B2D0613082F7 CRC64;
  Query Match      48.5%; Score 49; DB 10; Length 754;
  Best Local Similarity 53.8%; Pred. No. 32;
  Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAP 13
  ||| | |||
Db 665 WLQPEQGQEGYYP 677
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Search completed: December 23, 2002, 07:29:44
Job time : 10.0504 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 : Search time 4.29457 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-3

Perfect score: 51

Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	8	21	AA197231
2	51	100.0	8	22	AA13139
3	51	100.0	8	22	AA13139
4	51	100.0	8	23	AA13139
5	51	100.0	117	21	AA197235
6	51	100.0	117	22	AA13143
7	51	100.0	117	22	AA13143
8	51	100.0	117	23	AA13143
9	51	100.0	117	23	AA13143
10	51	100.0	136	22	AA13145
					Complementary dete
					Humanised antibody
					VEGF antagonist an
					Heavy chain comple
					Variable heavy cha
					Humanised antibody
					VEGF antagonist an
					Antigen-binding pr
					Antigen-binding pr
					Chimeric p1C11 hea

11	51	100.0	136	22	AA13145	VEGF antagonist an
12	51	100.0	238	23	AA13145	Antigen-binding pr
13	51	100.0	240	23	AA13145	Antigen-binding pr
14	39	76.5	11	17	AA13145	VLA-4 binding pept
15	38	74.5	120	12	AA13145	Control fusion pro
16	38	74.5	322	23	AA13145	Beta vulgaris RNA
17	38	74.5	364	21	AA13145	Arabidopsis thalia
18	38	74.5	364	21	AA13145	Arabidopsis thalia
19	38	74.5	365	21	AA13145	Arabidopsis thalia
20	38	74.5	365	21	AA13145	Arabidopsis thalia
21	38	74.5	387	21	AA13145	Arabidopsis thalia
22	38	74.5	387	21	AA13145	Arabidopsis thalia
23	38	74.5	564	21	AA13145	Arabidopsis thalia
24	38	74.5	738	21	AA13145	Arabidopsis thalia
25	38	74.5	745	21	AA13145	Arabidopsis thalia
26	37	72.5	248	22	AA13145	Drosophila melanog
27	37	72.5	264	20	AA13145	Fragment of human
28	37	72.5	279	22	AA13145	Human protein sequ
29	37	72.5	300	22	AA13145	Drosophila melanog
30	37	72.5	485	22	AA13145	Novel human diagno
31	37	72.5	562	23	AA13145	Neisseria meningit
32	37	72.5	562	23	AA13145	Neisseria meningit
33	37	72.5	562	23	AA13145	Neisseria meningit
34	37	72.5	633	21	AA13145	Human secreted pro
35	36	70.6	97	17	AA13145	Salmonella sero gp
36	36	70.6	191	23	AA13145	Listeria monocytog
37	36	70.6	307	22	AA13145	Drosophila melanog
38	36	70.6	441	23	AA13145	Herbicidally activ
39	36	70.6	525	21	AA13145	Raccoonpox virus B
40	36	70.6	591	12	AA13145	Gamma glutamyl tra
41	36	70.6	624	19	AA13145	Thyroid peroxidase
42	36	70.6	626	19	AA13145	Thyroid peroxidase
43	36	70.6	663	19	AA13145	Thermotoga maritim
44	36	70.6	666	19	AA13145	Thermotoga neapoli
45	36	70.6	680	18	AA13145	Thermotoga maritim

ALIGNMENTS

RESULT 1

AA197231

ID AA197231 standard; Protein; 8 AA.

XX

AC AA197231;

XX

DT 19-DEC-2000 (first entry)

XX

XX Complementary determining region (CDRH3) of anti-SI(KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR;

XX VEGF; vascular endothelial growth factor; KDR;

XX Kinase insert domain containing receptor; multivalent; monovalent;

XX Humanised antibody; chimeric antibody; tumour; diastomy; triastomy;

XX glioblastoma multiforme; hemangioblastoma; AIDS;

XX central nervous system neoplasms; AIDS associated Karposi's sarcoma;

XX acquired immune deficiency syndrome; AIDS; human.

OS Homo sapiens.

OS Synthetic.

XX

PN WO200004777-A1.

XX

PD 03-AUG-2000.

XX

PF 28-JAN-2000; 2000WO-US02180.

XX

PR 29-JAN-1999; 99US-0117726.

XX

PR 29-JAN-1999; 99US-0240736.

XX

PA (IMCL-) INCLONE SYSTEMS INC.

XX

PI Zhu Z, Witte L;

XX WPI; 2000-505966/45.
 DR N-PSDB; AAA53763.
 XX Novel immunoglobulin molecules binding kinase insert domain-containing
 PT receptor with the same affinity as vascular endothelial growth factor,
 PT used to reduce tumour growth
 XX
 PS Claim 3; Page 50; 55pp; English.
 XX
 CC New immunoglobulin molecules are described that bind kinase insert
 CC domain-containing receptor (KDR) with a comparable affinity to human
 CC vascular endothelial growth factor (VEGF). The antibodies neutralise
 CC KDR activation. The immunoglobulin may be a multivalent single
 CC chain antibody, a monovalent single chain antibody, a diabody, a
 CC triabody, a humanised antibody or a chimerised antibody.
 CC The immunoglobulin molecules bind specifically to an
 CC extracellular domain of the KDR receptor with the same affinity as
 CC VEGF. Overexpression of VEGF has been implicated in a number of
 CC human tumour cell lines including glioblastoma multiforme,
 CC hemangioblastoma, central nervous system neoplasms and AIDS
 CC associated kaposi's sarcoma. The antibodies therefore have
 CC applications in treating these conditions. This sequence encodes a
 CC preferred heavy chain complementarity determining region of the
 CC immunoglobulins of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDYEGY 8
 |||||
 Db 1 YGDYEGY 8

RESULT 2
 AAEL13139
 ID AAEL13139 standard; peptide; 8 AA.
 AC AAEL13139;
 XX
 DT 28-JAN-2002 (first entry)
 DE Humanised antibody murine heavy chain hypervariable region (VH) CDR3.
 XX
 KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytosolic; heavy chain hypervariable region; VH; myelocytic leukaemia;
 KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
 KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse;
 XX
 OS Mus sp.
 XX
 PN WO200174296-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10504.
 XX
 PR 31-MAR-2000; 2000US-0540770.
 XX
 XX (IMCL-) IMCLONE SYSTEMS INC.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Witte L, Rafil S;
 XX
 XX WPI; 2001-662942/76.
 DR N-PSDB; AAD21665.
 XX
 PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with
 PT an antagonist of a vascular endothelial growth factor receptor -

XX Claim 8; Page 14; 68pp; English.
 PS
 CC The invention relates to a method for inhibiting the growth of non-solid
 CC tumour cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to
 CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
 CC antibody murine heavy chain hypervariable region (VH) CDR-3 used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDYEGY 8
 |||||
 Db 1 YGDYEGY 8

RESULT 3
 AAB82705
 ID AAB82705 standard; Peptide; 8 AA.
 AC AAB82705;
 XX
 DT 15-OCT-2001 (first entry)
 DE VEGF antagonist antibody IMC-1C11 VH CDR-3.
 XX
 KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
 KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
 KW antitumour; neoplasm; collagen-vascular disease; autolimmune disease;
 KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
 KW colon carcinoma; ovarian carcinoma; neuroblastoma;
 KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
 KW complementarity determining region.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN WO200154723-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US02839.
 XX
 PR 28-JAN-2000; 2000US-0178791.
 PR 31-MAR-2000; 2000US-0539692.
 XX
 XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Kerbel R;
 XX
 DR WPI; 2001-514531/56.
 XX
 PT Treating or controlling an angiogenic dependent condition (e.g. a
 PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
 PT administering a combination of an antiangiogenic molecule and a
 PT chemotherapeutic agent -
 XX
 XX Disclosure; Page 37; 42pp; English.
 PS

CC The present sequence is that of complementarity determining region
 CC 3 of the heavy chain variable region (see also AAB82701) of
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,
 CC or a fragment of it, can be used as an anti-angiogenic molecule,
 CC together with a chemotherapeutic acid, for the treatment of an
 CC angiogenic dependent condition in a mammal, especially a human.
 CC The invention relates generally to a method of treating or
 CC controlling an angiogenic dependent condition by administering an
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
 CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The anti-angiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
 |||||
 Db 1 YGDIYEGY 8

RESULT 4
 AAU74408
 ID AAU74408 standard; peptide; 8 AA.

AC AAU74408;

DT 26-MAR-2002 (first entry)

DE Heavy chain complementarity determining region H3 (CDRH3).

XX Complementarity determining region; CDR; CDRH3; antigen; cytostatic;
 KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
 KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
 KW antibody heavy chain variable domain.

XX Mus sp.

OS WO200190192-A2.

PN 29-NOV-2001.

PP 24-MAY-2001; 2001WO-US16924.

PR 24-MAY-2000; 2000US-206749P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

XX WPI; 2002-106189/14.

DR N-PSDB; AAS20279.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides

XX Claim 55; Page 56; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This peptide sequence represents the heavy chain variable domain
 CC complementarity determining region H3 (CDRH3) incorporated into an
 CC antigen-binding protein described in the method of the invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
 |||||
 Db 1 YGDIYEGY 8

RESULT 5

AA97235

ID AA97235 standard; Protein; 117 AA.

XX AA97235;

DT 19-DEC-2000 (first entry)

DE Variable heavy chain fragment of anti-SI(KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR;

KW VEGF; vascular endothelial growth factor; KDR;

KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diabody; triabody;

KW glioblastoma multiforme; hemangioblastoma; AIDS;

KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;

KW acquired immune deficiency syndrome; AIDS; human.

OS Homo sapiens.

OS Synthetic.

XX WO200044777-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US02180.

XX 29-JAN-1999; 99US-0117726.

XX 29-JAN-1999; 99US-0240736.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z, Witte L;

XX WPI; 2000-505966/45.

DR N-PSDB; AAA53767.

XX Novel immunoglobulin molecules binding kinase insert domain-containing
 PT receptor with the same affinity as vascular endothelial growth factor,
 PT used to reduce tumour growth

XX Claim 4; Page 50-51; 55pp; English.

XX New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumor cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.

XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 51; DB 21; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
DB 99 YGDIYEGY 106
|||||

RESULT 6
AAE13143
ID AAE13143 standard; Protein: 117 AA.
XX AAE13143
XX AAE13143
XX AAE13143
DT 28-JAN-2002 (first entry)
XX Humanised antibody heavy chain fragment.
DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.
XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX WO200174296-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10504.
XX 31-MAR-2000; 2000US-0540770.
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR.) CORNELL RES FOUND INC.
PI Witte L; Rafii S;
XX WPI; 2001-662942/76.
DR N-PSDB; AAD21669.
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX Claim 8; Page 15; 68pp; English.
PS
XX The invention relates to a method for inhibiting the growth of non-solid
CC tumor cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse

CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain fragment used in the exemplification of the
CC invention.

XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 51; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
DB 99 YGDIYEGY 106
|||||

RESULT 7
AAB82709
ID AAB82709 standard; Protein: 117 AA.
XX AAB82709
XX AAB82709
DT 15-OCT-2001 (first entry)
XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.
DE
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX

FH Key Location/Qualifiers
FT Region 26..35
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 99..106
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX WO200154723-A1.
XX 02-AUG-2001.
XX 29-JAN-2001; 2001WO-US02839.
XX 28-JAN-2000; 2000US-0178791.
XX 31-MAR-2000; 2000US-0539692.
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX Kerbel R;
XX WPI; 2001-514531/56.
DR N-PSDB; AAH26405.
XX Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent

XX PS Disclosure; Page 38; 42pp; English.

XX CC The present sequence is that of the heavy chain variable region of

CC IMC-1C11, a mouse-human chimeric antibody that has vascular

CC endothelial growth factor (VEGF) antagonist activity. The antibody,

CC or a fragment of it, can be used as an anti-angiogenic molecule,

CC together with a chemotherapeutic acid, for the treatment of an

CC angiogenic dependent condition in a mammal, especially a human.

CC The invention relates generally to a method of treating or

CC controlling an angiogenic dependent condition by administering an

CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a

CC regression or arrest of the condition while minimising or

CC preventing significant toxicity of the chemotherapeutic agent.

CC The anti-angiogenic molecule inhibits or blocks the action of a

CC vascular endothelium survival factor such as VEGF or its receptor,

CC and is especially IMC-1C11. Conditions that can be treated include

CC a neoplasm, a collagen-vascular disease or an autoimmune disease,

CC especially a solid tumour, including breast carcinoma, lung

CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,

CC ovarian carcinoma, neuroblastoma, central nervous system tumour,

CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 22; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8

Db 99 YG DYEGY 106

RESULT 8

AAU74412

ID AAU74412 standard; peptide; 117 AA.

XX AC AAU74412;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein heavy chain variable domain (VH) #1.

XX KW Antigen-binding protein; antibody heavy chain variable domain;

KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.

OS Mus sp.

PN WO200190192-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX DR WPI; 2002-106189/14.

DR N-PSDB; AAS20283.

XX CC New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX PS Claim 57; Page 57; 64pp; English.

XX CC The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which

CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

CC light chain constant domain (Ch domain), and P2 has an antigen-binding

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC neutralising the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and

CC its ligand; promoting interactions between immune cells and target cells;

CC and in vivo and in vitro for investigative, diagnostic or treatment

CC methods. The design of (I) provides for efficient production so that

CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous

CC and in tetrameric form. The heavy chain constant domains which constitute

CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

CC antibody and which provide other antibody functions can be present. There

CC is no requirement for processing in vitro to obtain the complete product.

CC This sequence represents a heavy chain variable domain (VH) incorporated

CC into Fv, an engineered protein containing a heavy chain variable domain

CC and a light chain variable domain in one polypeptide chain, described in

CC the method of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.53;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8

Db 99 YG DYEGY 106

RESULT 9

AAU74417

ID AAU74417 standard; peptide; 117 AA.

XX AC AAU74417;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein heavy chain variable domain (VH) #2.

XX KW Antigen-binding protein; antibody heavy chain variable domain;

KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.

OS Mus sp.

PN WO200190192-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX DR WPI; 2002-106189/14.

DR N-PSDB; AAS20288.

XX CC New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of

PT two polypeptides and two second polypeptides

XX PS Claim 61; Page 60; 64pp; English.

XX CC The invention describes an antigen-binding protein (I) comprising a

CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This sequence represents a heavy chain variable domain (VH) incorporated
 CC into Fv, an engineered protein containing a heavy chain variable domain
 CC and a light chain variable domain in one polypeptide chain, described in
 CC the method of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 51; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.53; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

Qy 1 YGDIYEGY 8

Db 99 YGDIYEGY 106

|||||

RESULT 10

AAE13145

ID AAE13145 standard; Protein; 136 AA.

XX AAE13145;

28-JAN-2002 (first entry)

DE Chimeric p1c11 heavy chain fragment.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
 KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
 KW human; p1c11 vector.

XX Chimeric - Homo sapiens.

OS Chimeric - Unidentified.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= leader_peptide

FT Region 45..54

FT Region /note= "Mature chimeric p1c11 heavy chain fragment"

FT Region /label= CDR_H1

FT Region /label= CDR_H2

FT Misc-difference 84

FT /note= "Residue 'O' is present at this location in the
 sequence shown in fig-11 of the specification"

FT Misc-difference 101

FT /note= "Residue 'O' is present at this location in the
 sequence shown in fig-11 of the specification"

FT Region 119..125

FT Region /label= CDR_H3

XX WO200174296-A2.

PN 11-OCT-2001.

XX

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

PR (IMCL-) IMCLONE SYSTEMS INC.

PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.

DR N-PSDB; AAD21682.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow

XX tumors such as leukemias or multiple myeloma comprises treatment with

XX an antagonist of a vascular endothelial growth factor receptor -

XX Example 3; Fig 11; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid

XX tumor cells that are stimulated by a ligand of vascular endothelial

XX growth factor receptor (VEGFR) in mammals particularly humans. The method

XX involves treating the mammals with humanised VEGFR monoclonal antibodies

XX (antagonists). Humanised monoclonal antibody comprises humanised mouse

XX variable region joined to human constant region, where the humanised

XX mouse variable region contains mouse complementarity determining region

XX (CDR) grafted into human variable region. The method is useful for

XX treating leukaemias such as acute or chronic myelocytic leukaemia, acute

XX or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,

XX multiple myelomas and lymphoid cells, particularly those related to

XX non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric

XX p1c11 heavy chain fragment which is used for the construction of chimeric

XX p1c11 IgG expression vector. Chimeric p1c11 heavy chain contains cloned

XX variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant

XX domain (CH).

XX Sequence 136 AA;

Query Match 100.0%; Score 51; DB 22; Length 136;

Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDIYEGY 8

Db 118 YGDIYEGY 125

|||||

RESULT 11

AAE82701

ID AAE82701 standard; Protein; 136 AA.

XX AAE82701;

XX 15-OCT-2001 (first entry)

DE VEGF antagonist antibody IMG-1C11 heavy chain variable region.

XX IVC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;

XX vascular endothelial growth factor; angiogenesis; antiangiogenic;

XX antitumour; neoplasm; collagen-vascular disease; autoimmune disease;

XX tumour; breast carcinoma; lung carcinoma; prostate carcinoma;

XX colon carcinoma; ovarian carcinoma; neuroblastoma;

XX glioblastoma multiforme; melanoma; therapy; heavy chain.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= signal_peptide

FT Region 20..136

FT Region /label= Mature_protein

FT Region 45..54

```

FT FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 59...85
FT FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 118...125
FT FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
XX WO200154723-A1.
XX
XX PD 02-AUG-2001.
XX
XX PF 29-JAN-2001; 2001WO-US02839.
XX
XX PR 28-JAN-2000; 2000US-0178791.
XX PR 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Kerbel R;
XX
XX WPI; 2001-514531/56.
XX N-PSDB; AAH26413.
XX
XX Treating or controlling an angiogenic dependent condition (e.g. a
XX neoplasm, collagen-vascular or autoimmune disease) in mammal by
XX administering a combination of an antiangiogenic molecule and a
XX chemotherapeutic agent -
XX
XX PS Disclosure; Fig 1; 42pp; English.
XX
XX The present sequence is that of the heavy chain variable region of
XX IMC-1c11, a mouse-human chimeric antibody that has vascular
XX endothelial growth factor (VEGF) antagonist activity. The antibody,
XX or a fragment of it, can be used as an anti-angiogenic molecule,
XX together with a chemotherapeutic acid, for the treatment of an
XX angiogenic dependent condition in a mammal, especially a human.
XX The invention relates generally to a method of treating or
XX controlling an angiogenic dependent condition by administering an
XX anti-angiogenic molecule and a chemotherapeutic agent, to produce a
XX regression or arrest of the condition while minimising or
XX preventing significant toxicity of the chemotherapeutic agent.
XX The anti-angiogenic molecule inhibits or blocks the action of a
XX vascular endothelium survival factor such as VEGF or its receptor,
XX and is especially IMC-1c11. Conditions that can be treated include
XX a neoplasm, a collagen-vascular disease or an autoimmune disease,
XX especially a solid tumour, including breast carcinoma, lung
XX carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
XX ovarian carcinoma, neuroblastoma, central nervous system tumour,
XX neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
XX Sequence 136 AA;
XX
XX Query Match 100.0%; Score 51; DB 22; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 0.63;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YGDEYEGY 8
XX
XX Db 118 YGDEYEGY 125
XX
XX RESULT 12
XX AAU74420
XX ID AAU74420 standard; Protein; 238 AA.
XX
XX AAU74420;
XX
XX AC
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Antigen-binding protein, single chain variable fragment version #2.

```

```

XX
XX KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
XX cytotstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
XX KW vascular endothelial growth factor receptor; VEGF;
XX cell proliferation inhibitor.
XX
XX OS Mus sp.
XX OS Synthetic.
XX
XX FH Key
XX FH Location/Qualifiers
XX FT 1..117
XX FT /label= VH
XX FT /note= "Heavy chain variable domain. Specifically
XX FT claimed in claim 61"
XX
XX FT 118..132
XX FT /label= Linker
XX FT /note= "15 amino acid linker joins the VH and VL
XX FT regions of the single chain variable fragment
XX FT protein. Encoded by AAS20285"
XX
XX FT 133..238
XX FT /label= VL
XX FT /note= "Light chain variable domain. Specifically
XX FT claimed in claim 61"
XX
XX WO200190192-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
XX
XX 24-MAY-2000; 2000US-206749p.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2002-106189/14.
XX
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
XX tumour growth and for inhibiting angiogenesis, comprises a complex of
XX two polypeptides and two second polypeptides -
XX
XX Claim 63; Page 62-63; 64pp; English.
XX
XX The invention describes an antigen-binding protein (I) comprising a
XX complex of two polypeptides (P1) and two second polypeptides (P2) which
XX are stably associated in an immunoglobulin like complex. P1 has an
XX antigen-binding site located to the N terminus of immunoglobulin (Ig)
XX light chain constant domain (CL domain), and P2 has an antigen-binding
XX site located to the N terminus of the CH1 domain. (I) is useful for:
XX neutralising the activation of a vascular endothelial growth factor
XX (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
XX reducing endothelial cell proliferation; inhibiting VEGF induced
XX migration of human leukaemia cells; blocking interaction of a protein and
XX its ligand; promoting interactions between immune cells and target cells;
XX in vivo and in vitro for investigative, diagnostic or treatment
XX methods. The design of (I) provides for efficient production so that
XX substantially all of the antigen-binding proteins produced are assembled
XX in the desired configuration. (I) is bivalent and bispecific, homogeneous
XX and in tetrameric form. The heavy chain constant domains which constitute
XX the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
XX antibody and which provide other antibody functions can be present. There
XX is no requirement for processing in vitro to obtain the complete product.
XX This is the amino acid sequence of a single chain variable fragment
XX (scFv), an engineered protein containing a variable light and variable
XX heavy domain on one polypeptide, described in the method of the
XX invention.
XX
XX SQ Sequence 238 AA;
XX
XX Query Match 100.0%; Score 51; DB 23; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 1.1;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 YGDEYEGY 8
 DB 99 YGDEYEGY 106

RESULT 13
 AAU74419 standard; Protein; 240 AA.
 ID AAU74419;
 XX AAU74419;
 AC AAU74419;
 XX 26-MAR-2002 (first entry)
 DT DT
 XX Antigen-binding protein, single chain variable fragment version #1.
 DE Antigen-binding protein; single chain variable fragment; scFv; antigen;
 XX cytoskeletal; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 KW cell proliferation inhibitor.
 XX
 OS Mus sp.
 OS Synthetic
 XX
 XX Key Location/Qualifiers
 XX Region 1..117
 FT /label= VH
 FT /note= "Heavy chain variable domain. Specifically
 FT claimed in claim 57"
 FT Region 118..132
 FT /label= Linker
 FT /note= "15 amino acid linker joins the VH and VL
 FT regions of the single chain variable
 FT fragment protein. Encoded by AAS20285"
 FT Region 133..240
 FT /label= VL
 FT /note= "Light chain variable domain. Specifically
 FT claimed in claim 57"
 XX
 XX WO200190392-A2.
 XX
 XX 29-NOV-2001.
 PD
 XX 24-MAY-2001; 2001WO-US16924.
 XX
 XX 24-MAY-2000; 2000US-206749P.
 XX
 XX (IMCL-) IMCLONE SYSTEMS INC.
 XX
 XX Zhu Z;
 XX
 XX WPI; 2002-106189/14.
 XX
 PT New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides -
 XX
 XX Claim 63; Page 62; 64pp; English.
 XX
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This is the amino acid sequence of a single chain variable fragment
 CC (scFv), an engineered protein containing a variable light and variable
 CC heavy domain on one polypeptide, described in the method of the
 CC invention.

XX SQ Sequence 240 AA;

Query Match 100.0%; Score 51; DB 23; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDEYEGY 8

DB 99 YGDEYEGY 106

RESULT 14

AAR92576

ID AAR92576 standard; peptide; 11 AA.

XX

XX AAR92576;

XX

DT 10-SEP-1996 (first entry)

XX

XX VLA-4 binding peptide #39.

XX

KW VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR;
 KW alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis;
 KW complementarity determining region; inflammatory brain disorder; therapy;
 KW multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis;
 KW AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases;
 KW rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

XX

XX

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CC arthritis, transplant rejection, tumour metastases and myocardial
CC ischaemia. These sequences can also be labelled, and can then be used
CC for in vivo or in vitro diagnosis, such as monitoring inflammatory
CC responses, isolating leucocytes, in assays for inhibitors of VLA-4/VCAM-1
CC interactions and imaging sites of inflammation.
XX

SQ Sequence 11 AA;

Query Match 76.5%; Score 39; DB 17; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
 |||||
DB 3 YYGNYGGY 10

RESULT 15

AAR13721
ID AAR13721 standard; Protein; 120 AA.

AC AAR13721;

DT 06-NOV-1991 (first entry)

DE Control fusion protein putative binding site.

KW Heterofunctional; totally synthetic affinity reagents; TSAR.

XX Synthetic.

PN W09112328-A.

XX 22-AUG-1991.

PF 14-FEB-1991; 91WO-US01013.

PR 15-FEB-1990; 90US-0480420.

PA (FOWL/) FOWLKES D M.

PI Fowlkes D, Kay BK;

DR WPI; 1991-267139/36.

DR N-PSDB; AAQ13360.

PT Prodn. of hetero-functional binding fusion proteins - used for in

PT vitro and in vivo applications, e.g. diagnosis and vaccine prodn.

PS Disclosure; Fig 2; 81pp; English.

XX This amino acid sequence codes for the N-terminal end of the
CC control fusion protein. It was obt'd. from the DNA and makes up the
CC putative binding domain of the control fusion protein. The fusion
CC proteins, termed Totally Synthetic Affinity Reagents (TSARs) are
CC useful for in vitro and in vivo applications that make use of
CC binding regions of antibodies, DNA binding proteins, adhesive
CC proteins, etc. e.g. in the field of biomedicine, bio-regulation and
CC control. Also in the prodn. of vaccines, (immunogens) in separations
CC and purifications, and in diagnostics. The method is quick, simple,
CC efficient and relatively inexpensive. A great diversity of binding
CC characteristics can be obt'd. There is no need for detailed
CC knowledge of the function of portions of the binding sequence or
CC the amino acids that are involved in ligand binding in order to
CC produce the TSARs. See also AAR13722.

SQ Sequence 120 AA;

Query Match 74.5%; Score 38; DB 12; Length 120;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8

Db 99 YYDYEGF 106
 ||| |||||

Search completed: December 23, 2002, 07:25:04
Job time : 5.29457 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 1.44186 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-3

Perfect score: 51

Sequence: 1 YG DYEGY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	76.5	11	3	US-08-467-580-43
2	39	76.5	11	5	PCT-US95-08516-43
3	36	70.6	525	4	US-09-113-750A-35
4	36	70.6	663	4	US-09-134-078-61
5	36	70.6	680	4	US-09-134-078-25
6	36	70.6	933	2	US-08-313-200-1
7	36	70.6	933	5	PCT-US93-03837-1
8	35	68.6	1507	6	5268270-2
9	34	66.7	116	2	US-08-888-365-12
10	34	66.7	139	4	US-09-136-315-2
11	34	66.7	139	4	US-09-136-315-6
12	34	66.7	660	4	US-09-134-001C-3350
13	33.5	65.7	261	2	US-07-857-224B-61
14	33	64.7	11	3	US-08-467-580-42
15	33	64.7	11	5	PCT-US95-08516-42
16	33	64.7	371	1	US-08-225-477B-8
17	33	64.7	371	5	PCT-US95-04353-8
18	33	64.7	389	4	US-09-055-765-13
19	33	64.7	400	4	US-09-264-097-6
20	33	64.7	402	4	US-09-055-765-14
21	33	64.7	405	4	US-09-291-023A-20
22	33	64.7	485	2	US-08-446-803-1
23	33	64.7	485	2	US-08-446-803-2
24	33	64.7	485	2	US-08-861-837-1
25	33	64.7	485	2	US-08-861-837-2
26	33	64.7	485	2	US-08-600-908A-12
27	33	64.7	485	3	US-08-683-838A-12

28	33	64.7	485	3	US-08-600-656-1	Sequence 1, Appli
29	33	64.7	485	3	US-08-600-656-2	Sequence 2, Appli
30	33	64.7	485	3	US-08-600-656-7	Sequence 7, Appli
31	33	64.7	485	4	US-09-170-670-1	Sequence 1, Appli
32	33	64.7	485	4	US-09-170-670-2	Sequence 2, Appli
33	33	64.7	485	4	US-09-170-670-6	Sequence 6, Appli
34	33	64.7	485	4	US-09-170-670-7	Sequence 7, Appli
35	33	64.7	485	4	US-09-170-670-8	Sequence 8, Appli
36	33	64.7	485	4	US-09-193-068-1	Sequence 1, Appli
37	33	64.7	485	4	US-09-193-068-2	Sequence 2, Appli
38	33	64.7	485	4	US-09-193-068-6	Sequence 6, Appli
39	33	64.7	485	4	US-09-193-068-7	Sequence 7, Appli
40	33	64.7	485	4	US-09-193-068-8	Sequence 8, Appli
41	33	64.7	485	4	US-09-183-412-1	Sequence 1, Appli
42	33	64.7	485	4	US-09-183-412-2	Sequence 2, Appli
43	33	64.7	485	4	US-09-183-412-6	Sequence 6, Appli
44	33	64.7	485	4	US-09-183-412-7	Sequence 7, Appli
45	33	64.7	485	4	US-09-183-412-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-467-580-43
; Sequence 43, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; EARLIER FILING DATE: 1995-06-06
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: derived from VCAM-1
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
US-08-467-580-43

Query Match 76.5%; Score 39; DB 3; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YG DYEGY 8
Db 3 YG NYGGY 10

RESULT 2
PCT-US95-08516-43
; Sequence 43, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATHENA NEUROSCIENCES, INC.
; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
; STREET: 800 Gateway Blvd.
; CITY: South San Francisco
; STATE: CA

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08516
FILING DATE: 10-JUL-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,055
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 002010-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-3620
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-08516-43

Query Match: 76.5%; Score 39; DB 5; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDEYEGY 8
||| |||
Db 3 YYGNYGGY 10

RESULT 3
US-09-113-750A-35
; Sequence 35% Application US/09113750A
; Patent No. 5294176
; GENERAL INFORMATION:
; APPLICANT: David E. Junker and Mark D. Cochran
; TITLE OF INVENTION: Recombinant Raccoonpox virus
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 110036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,750A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 55744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)262-0400
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-113-750A-35

Query Match: 70.6%; Score 36; DB 4; Length 525;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDEYEGY 8
| |||||
Db 71 YSGDYENY 78

RESULT 4
US-09-134-078-61
; Sequence 61, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-61

Query Match: 70.6%; Score 36; DB 4; Length 663;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDEYEGY 8
|| |||
Db 361 YYPDYDGF 368

RESULT 5
US-09-134-078-25
; Sequence 25, Application US/09134078
; Patent No. 6368844


```
;
;
; GENERAL INFORMATION:
; APPLICANT: Bylida, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
; US-09-134-078-25
;
; Query Match 70.6%; Score 36; DB 4; Length 680;
; Best Local Similarity 62.5%; Pred. No. 2.7e+02;
; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 YYGDIYEGY 8
; DB 378 YYPDYDGF 385
;
; RESULT 6
; US-08-313-200-1
; Sequence 1, Application US/08313200
; Patent No. 5998153
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,200
;
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20658.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 933 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Mature
; TISSUE TYPE: Thyroid gland(from people with Grave's
; TISSUE TYPE: disease)
; IMMEDIATE SOURCE:
; CLONE: pHTPO-2.8
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: join(1..3, 456..631)
; OTHER INFORMATION: /note= "TPO region within fusion
; OTHER INFORMATION: plasmid: TPO(delta4-455)"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
; OTHER INFORMATION: /note= "C-terminal truncation:
; OTHER INFORMATION: TPO(1-120)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..400
; OTHER INFORMATION: /note= "TPO epitopic region within
; OTHER INFORMATION: fusion protein: MBP-TPO (AA 1-400)"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..455
; OTHER INFORMATION: /note= "C-terminal truncation-
; OTHER INFORMATION: TPO(1-455) or N-terminal half of TPO"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..631
; OTHER INFORMATION: /note= "C-terminal truncation:
; OTHER INFORMATION: TPO(1-631)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 266..281
; OTHER INFORMATION: /note= "TPO epitopic or binding
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 376..631
; OTHER INFORMATION: /note= "TPO epitopic region within
; OTHER INFORMATION: fusion protein: MBP-TPO (AA 376-631)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: join(455..532, 590..933)
; OTHER INFORMATION: /note= "alternatively spliced
; OTHER INFORMATION: C-terminus of TPO"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 455..933
; OTHER INFORMATION: /note= "TPO C-terminus containing
; OTHER INFORMATION: binding region"
; FEATURE:
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NAME/KEY: Region
LOCATION: 456..631
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
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NAME/KEY: Region
LOCATION: 456..633
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 456..933
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 456..933
OTHER INFORMATION: /note= "TPO region within maltose
binding fusion protein"
FEATURE:
NAME/KEY: Region
LOCATION: 457..517
OTHER INFORMATION: /note= "non-reactive fragment"
FEATURE:
NAME/KEY: Region
LOCATION: 457..633
OTHER INFORMATION: /note= "TPO region within fusion
plasmid pMalTPO"
FEATURE:
NAME/KEY: Region
LOCATION: 457..933
OTHER INFORMATION: /note= "TPO binding region within
plasmid pMalTPO"
FEATURE:
NAME/KEY: Region
LOCATION: 465..933
OTHER INFORMATION: /note= "TPO binding region of
maltose binding region fusion construct"
FEATURE:
NAME/KEY: Region
LOCATION: 513..633
OTHER INFORMATION: /note= "recombinant TPO"
FEATURE:
NAME/KEY: Region
LOCATION: 517..630
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 517..633
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 573..633
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 590..611
OTHER INFORMATION: /note= "TPO region within maltose
binding fusion protein"
FEATURE:
NAME/KEY: Region
LOCATION: 590..615
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 590..675
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
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NAME/KEY: Region
LOCATION: 592..613
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 596..611
OTHER INFORMATION: /note= "Tpo region within fusion
protein"
FEATURE:
NAME/KEY: Region
LOCATION: 602..615
OTHER INFORMATION: /note= "TPO region containing
divergent sequences"
FEATURE:
NAME/KEY: Region
LOCATION: 611..615
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 631..933
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 632..933
OTHER INFORMATION: /note= "TPO region within maltose
binding fusion protein"
FEATURE:
NAME/KEY: Region
LOCATION: 633..768
OTHER INFORMATION: /note= "TPO binding or epitopic"
FEATURE:
Query Match 70.6%; Score 36; DB 2; Length 933;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YGDIYEGY 8
Db 466 YVGPYEGY 473
RESULT 7
PCT-US93-03837-1
; Sequence 1, Application PC/TUS9303837
; GENERAL INFORMATION:
; APPLICANT: Baker, Jr., James R.
; APPLICANT: Koenig, Ronald J.
; TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03837
; FILING DATE: 19930422
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewak, Anna M.
; REGISTRATION NUMBER: 33006
; REFERENCE/DOCKET NUMBER: 2115-00658PPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 641-1600
```

TELEFAX: (313) 641-0270
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 933 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Mature
; TISSUE TYPE: Thyroid gland (from people with Grave's
; TISSUE TYPE: disease)
; IMMEDIATE SOURCE:
; CLONE: pTPO-2.8
; PUBLICATION INFORMATION:
; AUTHORS: Kimura, S.
; AUTHORS: Kotani, T.
; AUTHORS: McBride, O. W.
; AUTHORS: Umeki, K.
; AUTHORS: Nakayama, T.
; AUTHORS: Ontaki, S.
; AUTHORS: Hirai, K.
; TITLE: Human thyroid peroxidase: Complete cDNA and
; TITLE: protein sequence, chromosome mapping, and
; TITLE: identification of two alternately spliced mRNAs
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 84
; PAGES: 5555-5559
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 3048
PCT-US93-03837-1

Query Match 70.6%; Score 36; DB 5; Length 933;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YG DYEGY 8
| | | | |
Db 466 YG PYEGY 473

RESULT 8
5268270-2
; Patent No. 5268270
; APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johnnes
; TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
; NEGATIVE HOST CELLS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/171.872
; FILING DATE: 01-JUL-1987
; SEQ ID NO: 2:
; LENGTH: 1507
5268270-2

Query Match 68.6%; Score 35; DB 6; Length 1507;
Best Local Similarity 62.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YG DYEGY 8
| | | | |
Db 110 YG QNGH 117

RESULT 9
US-08-888-366-12
; Sequence 12, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.

; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-366-12

Query Match 66.7%; Score 34; DB 2; Length 116;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YG DYEGY 8
| | | | |
Db 96 YG NYEW 103

RESULT 10
US-09-136-315-2
; Sequence 2, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILLIANO
; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
; TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
; FILE REFERENCE: 0010-0933-0
; CURRENT APPLICATION NUMBER: US/09/136.315B
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-136-315-2

Query Match 66.7%; Score 34; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
| | | | |
DB 119 YG SYGGF 126

RESULT 11

US-09-136-315-6
; Sequence 6, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
; TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
; FILE REFERENCE: 0010-0933-0
; CURRENT APPLICATION NUMBER: US/09/136,315B
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC DNA
US-09-136-315-6

Query Match 66.7%; Score 34; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
| | | | |
DB 119 YG SYGGF 126

RESULT 12

US-09-134-001C-3350
; Sequence 3350, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3350
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3350

Query Match 66.7%; Score 34; DB 4; Length 660;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
| | | | |
DB 123 YLGEYEGW 130

RESULT 13

US-07-857-224B-61
; Sequence 61, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Caenorhabditis elegans
; FEATURE: Protein kinase; Table 8 Column 69
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-61

Query Match 65.7%; Score 33.5; DB 2; Length 261;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 YG DYEGY 8
| | | | |
DB 14 YG DYEGY 21

RESULT 14

US-08-467-580-42
; Sequence 42, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055

;; EARLIER FILING DATE: 1994-07-11
;; NUMBER OF SEQ ID NOS: 163
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 42
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide
;; OTHER INFORMATION: derived from VCAM-1
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (1)
;; OTHER INFORMATION: ACETYLATION
US-08-467-580-42

Query Match 64.7%; Score 33; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 3 YGNYGAY 10

RESULT 15
PCT-US95-08516-42
; Sequence 42, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATHENA NEUROSCIENCES, INC.
; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
; STREET: 800 Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08516
; FILING DATE: 10-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/273,055
; FILING DATE: 11-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 002010-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-3620
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-08516-42

Query Match 64.7%; Score 33; DB 5; Length 11;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 3 YGNYGAY 10

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Job time : 2.44186 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 0.744186 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	51	100.0	8	10	US-09-865-198-3
3	51	100.0	117	10	US-09-976-787-7
4	51	100.0	117	10	US-09-976-787-23
5	51	100.0	117	10	US-09-865-198-7
6	51	100.0	117	10	US-09-865-198-22
7	51	100.0	238	10	US-09-976-787-29
8	51	100.0	238	10	US-09-865-198-28
9	51	100.0	240	10	US-09-976-787-28
10	51	100.0	240	10	US-09-865-198-27
11	37	72.5	335	10	US-09-821-687-11
12	37	72.5	633	10	US-09-821-687-10
13	36	70.6	663	9	US-10-121-032-61
14	36	70.6	680	9	US-10-121-032-25
15	35	68.6	214	10	US-09-925-299-990
16	34	66.7	652	10	US-09-815-242-5896
17	34	66.7	657	10	US-09-815-242-12135
18	34	66.7	657	10	US-09-815-242-13013
19	34	66.7	666	10	US-09-815-242-4933

20	34	66.7	677	10	US-09-815-242-10663	Sequence 10663, A
21	33	64.7	148	12	US-10-052-586-360	Sequence 360, App
22	33	64.7	197	9	US-09-918-543-13	Sequence 13, Appl
23	33	64.7	389	10	US-09-143-127-12	Sequence 12, Appl
24	33	64.7	389	12	US-10-036-507-13	Sequence 13, Appl
25	33	64.7	392	10	US-09-945-825-8	Sequence 8, Appl
26	33	64.7	402	10	US-09-143-127-10	Sequence 10, Appl
27	33	64.7	402	10	US-09-143-127-14	Sequence 14, Appl
28	33	64.7	402	12	US-10-036-507-14	Sequence 14, Appl
29	33	64.7	485	9	US-09-918-543-2	Sequence 2, Appl
30	33	64.7	485	9	US-09-918-543-4	Sequence 4, Appl
31	33	64.7	485	9	US-09-918-543-12	Sequence 12, Appl
32	33	64.7	485	9	US-09-795-211-1	Sequence 1, Appl
33	33	64.7	485	9	US-09-795-211-2	Sequence 2, Appl
34	33	64.7	485	10	US-09-769-864-1	Sequence 1, Appl
35	33	64.7	485	10	US-09-769-864-2	Sequence 2, Appl
36	33	64.7	485	10	US-09-769-864-6	Sequence 6, Appl
37	33	64.7	485	10	US-09-769-864-7	Sequence 7, Appl
38	33	64.7	485	10	US-09-769-864-8	Sequence 8, Appl
39	33	64.7	485	10	US-09-854-346-2	Sequence 2, Appl
40	33	64.7	485	10	US-09-854-346-4	Sequence 4, Appl
41	33	64.7	485	10	US-09-854-346-12	Sequence 12, Appl
42	33	64.7	485	10	US-09-854-346-13	Sequence 13, Appl
43	33	64.7	485	10	US-09-902-188A-1	Sequence 1, Appl
44	33	64.7	485	10	US-09-902-188A-2	Sequence 2, Appl
45	33	64.7	485	10	US-09-902-188A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-3
; Sequence 3, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-3
Query Match 100.0%; Score 51; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGDYEGY 8
Db 1 YGDYEGY 8
RESULT 2
US-09-865-198-3
; Sequence 3, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-3

Query Match 100.0%; Score 51; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 1 YG DYEGY 8

RESULT 3
US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 99 YG DYEGY 106

RESULT 4
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse

US-09-976-787-23

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 99 YG DYEGY 106

RESULT 5
US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 99 YG DYEGY 106

RESULT 6
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match 100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEGY 8
Db 99 YG DYEGY 106

RESULT 7
US-09-976-787-29

; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 51; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGYDYEY 8
| | | | | | | |
Db 99 YGYDYEY 106

RESULT 8

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 51; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGYDYEY 8
| | | | | | | |
Db 99 YGYDYEY 106

RESULT 9

US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 51; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGYDYEY 8
| | | | | | | |
Db 99 YGYDYEY 106

RESULT 10

US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 51; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGYDYEY 8
| | | | | | | |
Db 99 YGYDYEY 106

RESULT 11

US-09-821-687-11
; Sequence 11, Application US/09821687
; Patent No. US20020106724A1
; GENERAL INFORMATION:
; APPLICANT: MIKOSHIBA, KATSUHIKO
; APPLICANT: MIZUTANI, AKIHIRO
; TITLE OF INVENTION: RNA-BINDING PROTEIN
; FILE REFERENCE: 081356/0162
; CURRENT APPLICATION NUMBER: US/09/821,687
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-299812
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: m-hrRNP
US-09-821-687-11

Query Match 72.5%; Score 37; DB 10; Length 335;

Query Match 70.68; Score 36; DB 9; Length 680;

Best Local Similarity 62.5%; Pred. NO. 92;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGDIYEGY 8
Db 378 YPDYDGF 385

RESULT 15
US-09-925-299-990
; Sequence 990, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 990
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-990

Query Match 68.6%; Score 35; DB 10; Length 214;
Best Local Similarity 62.5%; Pred. NO. 46;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YGDIYEGY 8
Db 105 YGHYHGF 112

Search completed: December 23, 2002, 07:58:18
Job time : 0.744186 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 : Search time 1.5814 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-3
Perfect score: 51
Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	80.4	435	D81272	hypothetical prote
2	40	78.4	542	S63222	MPA43 protein - ye
3	40	78.4	616	1 S17WMT	methionine-tRNA li
4	40	78.4	1650	T18444	hypothetical prote
5	39	76.5	63	S44634	f22b7.4 protein -
6	38	74.5	595	B70402	hypothetical prote
7	38	74.5	660	E83656	methionyl-tRNA syn
8	38	74.5	3216	C90538	hypothetical prote
9	37	72.5	89	T19805	hypothetical prote
10	37	72.5	110	S13688	Ig heavy chain v r
11	37	72.5	154	A69012	conserved hypothet
12	37	72.5	271	S38115	hypothetical prote
13	37	72.5	542	B81910	probable ABC-trans
14	37	72.5	542	E81105	ABC transporter, A
15	37	72.5	564	T26053	hypothetical prote
16	37	72.5	633	T02673	heterogeneous nucl
17	37	72.5	730	A48832	cell surface glyco
18	37	72.5	1657	T19536	hypothetical prote
19	36	70.6	15	PH1366	Ig heavy chain DJ
20	36	70.6	120	A54256	Ig heavy chain V r
21	36	70.6	191	A1218	alpha-ribazole-5'-
22	36	70.6	191	AH1571	alpha-ribazole-5'-
23	36	70.6	252	A95071	amino acid ABC tra
24	36	70.6	441	T49265	hypothetical prote
25	36	70.6	565	G90518	5'-nucleotidase pr
26	36	70.6	587	F69631	gamma-glutamyltran
27	36	70.6	656	T03473	acetate-CoA ligase
28	36	70.6	669	D72278	endo-1,4-beta-mann
29	36	70.6	831	AB3513	ATPase virB4 homol

30	36	70.6	851	2 T51545	receptor protein k
31	36	70.6	868	2 A84518	probable receptor-
32	36	70.6	914	1 JN0550	iodide peroxidase
33	36	70.6	914	1 S07047	iodide peroxidase
34	36	70.6	933	1 OPHUIT	iodide peroxidase
35	35	68.6	113	2 G82387	hypothetical prote
36	35	68.6	126	2 S16280	Ig heavy chain (38
37	35	68.6	145	2 S03844	Ig heavy chain pre
38	35	68.6	186	2 A81210	dTDP-sugar epimera
39	35	68.6	188	2 H31066	hypothetical prote
40	35	68.6	201	2 H85910	unknown protein en
41	35	68.6	376	2 S69529	hypothetical prote
42	35	68.6	386	2 T14243	ubiquinol-cytochro
43	35	68.6	398	2 A75128	probable transamin
44	35	68.6	401	2 D71003	probable transamin
45	35	68.6	402	1 I61573	homeotic protein 1

ALIGNMENTS

RESULT 1

D81272

hypothetical protein Cj1295 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: D81272
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chl
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: D81272
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-435 <PAR>
A:Cross-references: GB:AL1139078; GB:AL111168; NID:g6968723; PIDN:CAB73722.1; PID:g696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1295
C:Superfamily: Campylobacter jejuni hypothetical protein Cj1295

Query Match 80.4%; Score 41; DB 2; Length 435;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGDYEGY 8
||||:|
Db 325 YGDYDGY 331

RESULT 2

S63222

MPA43 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N0875; protein YNL249c
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 06-Feb-1998
C:Accession: S63222; S61594
R:Sen-Gupta, M.; Gueldener, U.; Beinhauer, J.; Fiedler, T.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63220
A:Accession: S63222

A:Molecule type: DNA
A:Residues: 1-542 <SEN>
A:Cross-references: EMBL:Z71525; NID:g1302290; PID:e239640; PID:g1302291; MIPS:YNL249
A:Experimental source: strain S288C
R:Boles, E.; Hettmann, C.; Zimmermann, F.K.
submitted to the EMBL Data Library, December 1995
A:Reference number: S61594
A:Accession: S61594
A:Molecule type: DNA
A:Residues: 'YOD'/45, 'SR'/48, 'HGNLA'/54-542 <BOL>
A:Cross-references: EMBL:X94214; NID:g1122898; PID:e214032; PID:g1122899

C:Genetics:
A:Gene: SGD:MPX43
A:Cross-references: SGD:S0005193; MIPS:YNL249c
A:Map position: 14L

Query Match 78.4%; Score 40; DB 2; Length 542;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDYEG 7

Db 360 FYGDYEG 366

RESULT 3

SYTWT

methionine-tRNA ligase (EC 6.1.1.10) - Thermus aquaticus

N:Alternate names: methionyl-tRNA synthetase

C:Species: Thermus aquaticus

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002

C:Accession: A39517

R:Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T.

J. Biol. Chem. 266, 3268-3277, 1991

A:Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilus.

A:Reference number: A39517; MUID:91131636; PMID:1993699

A:Accession: A39517

A:Molecule type: DNA

A:Residues: 14516 <NUP>

A:Cross-references: GB:M64273; GB:J05744; NID:gl55135; PIDN:AAA27510.1; PID:gl55136

A:Experimental source: strain HB8, ATCC 27634

A>Note: the authors translated the codon TAC for residue 323 as Thr

C:Genetics:

A:Gene: mets

C:Superfamily: methionine-tRNA ligase

C:Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis

F:13,19,30/Active site: Tyr, His, Asp, Lys #status predicted

Query Match 78.4%; Score 40; DB 1; Length 616;

Best Local Similarity 85.7%; Pred. No. 29;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDYEG 7

Db 118 YGEGYEG 124

RESULT 4

T18444

hypothetical protein C0385c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C:Accession: T18444

R:Lawson, D.; Bowman, S.; Barrell, B.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z18935

A:Accession: T18444

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1650 <LAW>

A:Cross-references: EMBL:298547; NID:el325376; PID:el427940; PIDN:CAB1112.2

C:Genetics:

A:Map position: 3

A:Introns: 1597/3; 1625/3

A>Note: C0385c

Query Match 78.4%; Score 40; DB 2; Length 1650;

Best Local Similarity 75.0%; Pred. No. 78;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGDYEG 8

Db 525 YGDYEG 532

RESULT 5

S44634

f22b7.4 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997

C:Accession: S44634

R:Anderson, K.

submitted to the EMBL Data Library, March 1993

A:Description: Sequence of the C. elegans cosmid F22B7.

A:Reference number: S44628

A:Accession: S44634

A:Molecule type: DNA

A:Residues: 1-63 <AND>

A:Cross-references: EMBL:L12018; NID:gl56298; PID:gl56305

C:Genetics:

A:Introns: 21/2

Query Match 76.5%; Score 39; DB 2; Length 63;

Best Local Similarity 75.0%; Pred. No. 4.3;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGDYEG 8

Db 56 YGGYNGY 63

RESULT 6

B70402

hypothetical protein aq_1185 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000

C:Accession: B70402

V:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: B70402

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-595 <AQF>

A:Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07204.1; PID:g2983636; GB:AE00

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq_1185

C:Superfamily: Aquifex aeolicus hypothetical protein aq_1185

Query Match 74.5%; Score 38; DB 2; Length 595;

Best Local Similarity 85.7%; Pred. No. 62;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGDYEG 8

Db 159 YGDTGY 165

RESULT 7

E83656

methionyl-tRNA synthetase mets [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: E83656

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: E83656

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-660 <STO>

A:Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA03772.1; GSPDB:GN00153
A:Experimental source: strain C-125
C:Genetics:
A:Gene: mets
C:Superfamily: methionine-tRNA ligase

Query Match 74.5%; Score 38; DB 2; Length 660;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
DB 121 YLGDYEG 128

RESULT 8
C90538
hypothetical protein MYPV_2110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: C90538
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Status: preliminary
A:Accession: C90538
A:Molecule type: DNA
A:Residues: 1-3216 <KUR>
A:Cross-references: GB:AL445566; PID:g14089624; PIDN:CAC13384.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV_2110
A:Genetic code: SGC3

Query Match 74.5%; Score 38; DB 2; Length 3216;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
DB 1978 YYVDYEGF 1985

RESULT 9
T19805
hypothetical protein C37A5.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19805
R:White, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19180
A:Accession: T19805
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-89 <WIL>
A:Cross-references: EMBL:Z92828; PIDN:CAB07335.1; GSPDB:GN000019; CESP:C37A5.8
A:Experimental source: clone C37A5
C:Genetics:
A:Gene: CESP:C37A5.8
A:Map position: 1
A:Introns: 52/2

Query Match 72.5%; Score 37; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEGY 8
DB 61 YGYYGGY 68

C:Genetics:
A:Gene: MIPS:YK043c
A:Cross-references: SGD:S0001751
A:Map position: 11R
C:Superfamily: phosphoglycerate mutase; phosphoglycerate mutase homology

Query Match 72.5%; Score 37; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGDYEG 7
| | | | |
DB 102 YGDYEG 107

RESULT 13
B81910
Probable ABC-transporter ATP-binding protein NMA1409 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: B81910
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jorgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: B81910
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-542 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84649.1; PID:g738006
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1409
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 542;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEG 8
| | | | |
DB 528 YLGDYEG 535

RESULT 14
E81105
ABC transporter, ATP-binding protein NMB1240 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81105
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, W.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: E81105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-542 <TET>
A:Cross-references: GB:AE002472; GB:AE002098; NID:g7236475; PIDN:AAF41621.1; PID:g722648
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1240
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 542;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDYEG 8

DB 528 YLGDYEG 535
| | | | |
RESULT 15
T26053
Hypothetical protein W01C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26053
R:Sims, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20143
A:Accession: T26053
A:Status: preliminary; translated from GB/EMBL/DDBL
A:Molecule type: DNA
A:Residues: 1-564 <WIL>
A:Cross-references: EMBL:Z49969; PIDN:CAA90270.1; GSPDB:GN00020; CESP:W01C9.2
A:Experimental source: clone W01C9
C:Genetics:
A:Gene: CESP:W01C9.2
A:Map position: 2
A:Introns: 30/1; 64/1; 100/3; 124/3; 229/3; 272/3; 536/2
Query Match 72.5%; Score 37; DB 2; Length 564;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGDYEG 8
| | | | |
DB 67 YGDYEDY 73

Search completed: December 23, 2002, 07:31:35
Job time : 5.5814 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 : Search time 0.790698 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-3
Sequence: 51
1 YGDEYGY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	80.4	402	1 LHX5_HUMAN	Q9H2C1 homo sapien
2	41	80.4	402	1 LHX5_XENLA	P37137 xenopus lae
3	40	78.4	542	1 MP43_YEAST	P53583 saccharomyc
4	40	78.4	616	1 SYM_THERM	P23395 thermus the
5	39	76.5	63	1 YLW4_CAEEL	P34407 caenorhabdi
6	39	76.5	489	1 OCLN_FOTTR	Q28793 potorous tr
7	37	72.5	271	1 YK23_YEAST	P36136 saccharomyc
8	37	72.5	394	1 ASSY_METAC	Q8TNY5 methanosarc
9	37	72.5	399	1 LHX5_BRARE	P52889 brachydanio
10	37	72.5	446	1 SOX8_HUMAN	P57073 homo sapien
11	37	72.5	633	1 ROR_HUMAN	O43390 homo sapien
12	37	72.5	730	1 GL3A_DICDI	P34115 dictyosteli
13	36	70.6	587	1 GGT_BACSU	P54422 bacillus su
14	36	70.6	656	1 ACSA_RHOCA	O68040 rhodobacter
15	36	70.6	914	1 PERT_MOUSE	P35419 mus musculu
16	36	70.6	914	1 PERT_RAT	P14650 rattus norv
17	36	70.6	933	1 PERT_HUMAN	P07202 homo sapien
18	35	68.6	321	1 K6PF_PASMU	Q9CPH2 pasteurella
19	35	68.6	376	1 YO23_BPHP1	P51725 bacterioph
20	35	68.6	402	1 LHX5_MOUSE	P50459 mus musculu
21	35	68.6	405	1 LHX1_BRARE	Q90476 brachydanio
22	35	68.6	428	1 RF4_KLULA	P09806 kluyveromyc
23	35	68.6	464	1 XKDK_BACSU	P54331 bacillus su
24	35	68.6	685	1 ERT2_YEAST	P05453 saccharomyc
25	35	68.6	919	1 AMY_STRLI	Q05884 streptomyce
26	35	68.6	1532	1 IGA_NEIGO	P09790 neisseria g
27	35	68.6	2358	1 MKD2_SCHPO	Q9Y719 schizosacch
28	34	66.7	314	1 YG20_YEAST	P53257 saccharomyc
29	34	66.7	335	1 HTPX_ARCFU	O30004 archaeoglob
30	34	66.7	497	1 SYM_AQUAE	O67298 aquifex aeo
31	34	66.7	649	1 SYM_BACST	P23920 bacillus st
32	34	66.7	784	1 SX15_DROME	P40657 drosophila
33	34	66.7	972	1 UVRA_MYCTU	P94972 mycobacteri

34 34 66.7 3511 1 MYI5_MOUSE
35 33.5 65.7 101 1 GP33_BPSP1
36 33.5 65.7 1196 1 ABL1_CAEEL
37 33 64.7 211 1 PMGT_SCHPO
38 33 64.7 216 1 RPOE_MYCTU
39 33 64.7 265 1 LICD_HAEIN
40 33 64.7 350 1 EGSA_SULTO
41 33 64.7 351 1 EGSA_SULSO
42 33 64.7 367 1 HIS8_PARDE
43 33 64.7 370 1 MYOM_APLCA
44 33 64.7 379 1 SAT_PYRAB
45 33 64.7 384 1 GLF1_KLEPN

Q9GZ24 mus musculu
P06226 bacterioph
P03949 caenorhabdi
P36623 schizosacch
O05843 mycobacteri
P14184 haemophilus
P58460 sulfolobus
Q9UXE7 sulfolobus
Q51687 paracoccus
P15513 a myomoduli
P56863 pyrococcus
Q48485 klebsiella

ALIGNMENTS

RESULT 1
LHX5_HUMAN
ID LHX5_HUMAN STANDARD; PRT; 402 AA.
AC Q9H2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5.
GN LHX5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed-11137295;

RA Zhao Y., Hermesz E., Yarolin M.C., Westphal H.;

RT "Genomic structure, chromosomal localization and expression of the

RT human LIM-homeobox gene LHX5.";

RL Gene 260:95-101(2000).

CC -!- FUNCTION: Plays an essential role in the regulation of neuronal differentiation and migration during development of the central nervous system.

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- TISSUE SPECIFICITY: Expressed in fetal brain and in various regions of the adult central nervous system including the spinal cord, the thalamus, and the cerebellum.

CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.

CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS.

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EMBL: AF291181; AAG36963.1; -.

HSP: P06601; 1FJL.

TRANSFAC: T04180; -.

Genew; HGNC:14216; LHX5.

MIM; 605992; -.

InterPro: IPR001356; Homeobox.

InterPro: IPR001781; LIM.

Pfam; PF00046; homeobox; 1.

ProDom; PD000010; Homeobox; 1.

ProDom; PD000094; LIM; 2.

SMART; SM00389; HOX; 1.

SMART; SM00132; LIM; 2.

PROSITE; PS00027; HOMEBOX_1; 1.

PROSITE; PS00071; HOMEBOX_2; 1.

PROSITE; PS00478; LIM_DOMAIN_1; 2.

PROSITE; PS50023; LIM_DOMAIN_2; 2.

KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 402 AA; 44405 MW; E880138A1A3FCA2A CRC64;

Query Match 80.4%; Score 41; DB 1; Length 402;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEG 7
Db 278 YG DYQG 284

RESULT 2

LHX5_XENLA STANDARD; PRT; 402 AA.
ID LHX5_XENLA
AC P37137;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5) (XLIM-5) (XLIM-2A).
GN LHX5 OR LIM5 OR LIM2A OR LIM-2A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN NCBI_TaxID=8355;
RP SEQUENCE FROM N.A.
RX MEDLINE=95377545; PubMed=7649385;
RA Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.;
RT "The LIM class homeobox gene lhx5: implied role in CNS patterning in
Xenopus and zebrafish.";
RL Dev. Biol. 170:583-593(1995).
[2]
RP SEQUENCE OF 188-225 FROM N.A.
RX MEDLINE=92192449; PubMed=1347750;
RA Taira M., Jamrich M., Good P.J., Dawid I.B.;
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed
specifically in the organizer region of Xenopus gastrula embryos.";
RL Genes Dev. 6:356-366(1992).
CC -!- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS
SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
DIENCEPHALON
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
IONS.

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EMBL; L42546; AAA99464.1; -;
EMBL; Z11587; CAA77672.1; -;
HSSP; P06601; 1FJL.

TRANSFAC; T04209; -;
InterPro; IPR001356; Homeobox.

InterPro; IPR001781; LIM.
Pfam; PF00046; Homeobox; 1.

Pfam; PF00412; LIM; 2.
ProDom; PD000010; Homeobox; 1.

ProDom; PD000094; LIM; 2.
SMART; SM00389; HOX; 1.

SMART; SM00132; LIM; 2.
PROSITE; PS00478; LIM_DOMAIN_1; 2.

DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 402 AA; 44959 MW; A5852B94747E09F9 CRC64;

Query Match 80.4%; Score 41; DB 1; Length 402;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEG 7
Db 278 YG DYQG 284

RESULT 3

MP43_YEAST STANDARD; PRT; 542 AA.
ID MP43_YEAST
AC P53583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MP43 protein.
GN MP43 OR YNL249C OR N0875.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN NCBI_TaxID=4932;
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / FY1679;
RX MEDLINE=97377992; PubMed=9234673;
RA Sen-Gupta M., Gueldeger U., Beinhauer J.D., Fiedler T.A.,
RA Hegemann J.H.;
RT "Sequence analysis of the 33 kb long region between ORC5 and SU11
from the left arm of chromosome XIV from Saccharomyces cerevisiae.";
RL Yeast 13:849-860(1997).
[2]
RN SEQUENCE OF 41-542 FROM N.A.
RP STRAIN=ENVY.WA-1A;
RA Boles E., Hettmann C., Zimmermann F.K.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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EMBL; X96722; CAA65495.1; -;
EMBL; Z71525; CAA96156.1; -;
DR EMBL; X94214; CAA63905.1; -;
DR SGD; S0005193; MPA43.

FT CONFLICT 46 53
SQ SEQUENCE 542 AA; 61667 MW; 830AA8D4E95365AD CRC64;

Query Match 78.4%; Score 40; DB 1; Length 542;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG DYEG 7
Db 360 YG DYEG 366

QY 1 YG DYEG 7
Db 360 YG DYEG 366

RESULT 4
SYM_THETH

```
ID SYM_THETH STANDARD; PRT; 616 AA.
AC P23395;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (METS).
GN METG OR METS.
OS Thermus thermophilus.
OC Bacteria; Thermus; Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
ON NCBI_TaxID=274;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=911131636; PubMed=1993699;
RA Nureki O., Muramatsu T., Suzuki K., Kohda D., Matsuzawa H.,
RA Ohta T., Miyazawa T., Yokoyama S.;
RT "Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus
RT thermophilus HB8. Molecular cloning, primary-structure analysis,
RT expression in Escherichia coli, and site-directed mutagenesis.";
RL J. Biol. Chem. 266:3268-3277(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=20139706; PubMed=10673435;
RA Sugitara I., Nureki O., Ugaji-Yoshikawa Y., Kuwabara S., Shimada A.,
RA Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;
RT "The 2.0-A crystal structure of thermus thermophilus methionyl-tRNA
RT synthetase reveals two RNA-binding modules.";
RL Structure 8:197-208(2000).
CC -!- FUNCTION: IT IS PROBABLY ESSENTIAL FOR CELL SURVIVAL, BEING
CC REQUIRED NOT ONLY FOR ELONGATION OF PROTEIN SYNTHESIS BUT ALSO
CC FOR THE INITIATION OF ALL MRNA TRANSLATION THROUGH INITIATOR
CC TRNA(EMET) AMINOACYLATION.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -!- STRONG, TO CYSTEINYL-TRNA SYNTHETASE.
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-----
CC EMBL; M64273; AAA27510.1; -
CC PIR; A39517; SYTWMT.
CC PDB; 1A8H; 04-MAY-99.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA-bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA-bind; 1.
DR PRINTS; PR01041; TRNASYNTHMET.
DR TIGRFAMs; TIGR00398; metG; 1.
DR TIGRFAMs; TIGR00399; metG_C term; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW tRNA-binding; 3D-structure.
FT SITE 10 22 "HIGH" REGION.
FT SITE 297 301 "KMSKS" REGION.
FT BINDING 300 300 ATP (BY SIMILARITY).
FT DOMAIN 524 616 TRNA BINDING.
SQ SEQUENCE 616 AA; 70638 MW; 053982C62558B72A CRC64;

Query Match 78.4%; Score 40; DB 1; Length 616;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YG DYEG 7
DB 118 YG DYEG 124
|||||

RESULT 5
YLW4_CAEEL STANDARD; PRT; 63 AA.
ID YLW4_CAEEL
AC P34407;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F22B7.4 in chromosome III.
DE F22B7.4.
GN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Laetelle P., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sins M., Smaldon N., Smith A., Smith K., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Woulfdman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
-----
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-----
CC EMBL; L12018; AAA65461.1; -
CC DR WormPep; F22B7.4; CE00157.
KW Hypothetical protein.
SQ SEQUENCE 63 AA; 6803 MW; 2F7579C4907024B0 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 63;
Best Local Similarity 75.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YG DYEGY 8
DB 56 YG DYEGY 63
|||||

RESULT 6
OCLN_POTTR STANDARD; PRT; 489 AA.
ID OCLN_POTTR
AC Q28793;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Occludin.
GN OCLN.
OS Potorous tridactylus (Potoroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

CC Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous.
OX NCBI_TaxID=9310;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96181088; PubMed=8601611;
RA Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,
RA Itoh M., Yonemura S., Furuse M., Tsukita S.
RT "Interspecies diversity of the occludin sequence: cDNA cloning of
human, mouse, dog, and rat kangaroo homologues."
RL J. Cell Biol. 133:43-47(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE FORMATION AND REGULATION OF THE
CC TIGHT JUNCTION (TJ) PARACELLULAR PERMEABILITY BARRIER. INTERACTS
CC WITH ZO-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
CC EPITHELIAL AND ENDOTHELIAL CELLS.
CC -1- DOMAIN: THE C-TERMINAL IS CYTOPLASMIC AND IS IMPORTANT FOR
CC INTERACTION WITH ZO-1. NECESSARY FOR THE TIGHT JUNCTION
CC LOCALIZATION. INVOLVED IN THE REGULATION OF THE PERMEABILITY
CC BARRIER FUNCTION OF THE TIGHT JUNCTION (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ELL / OCCLUDIN FAMILY.
CC
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CC
CC EMBL: U46183; AAC48565.1; -
CC InterPro: IPR002958; Occludin.
CC Pfam: PF02168; Occludin; 1.
CC PRINTS: PR01258; OCCLUDIN.
CC TIGHT JUNCTION; Transmembrane; Coiled coil; Phosphorylation.
CC DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 52 74 POTENTIAL.
CC DOMAIN 75 112 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 113 137 POTENTIAL.
CC DOMAIN 138 147 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 148 172 POTENTIAL.
CC DOMAIN 173 222 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 223 244 POTENTIAL.
CC DOMAIN 245 489 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 407 434 TYR/GLY-RICH.
CC DOMAIN 407 434 COILED COIL (POTENTIAL).
CC SEQUENCE 489 AA; 54075 MW; 4F0CA45A41094860 CRC64;
Query Match 76.5%; Score 39; DB 1; Length 489;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YGDYEGY 8
DB 96 YYGNGY 103
RESULT 7
YK23_YEAST
ID YK23_YEAST STANDARD; PRT; 271 AA.
AC P36136;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hypothetical 31.0 kDa protein in GAPI-NAP1 intergenic region.
GN YKR043C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]

RP SEQUENCE FROM N.A.
RA Urrestazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL: Z28268; CAA82119.1; -
CC PIR: S38115; S38115.
CC SGD: S0001751; YKR043C.
CC InterPro: IPR001345; Pg/BPGM_mutase.
CC Pfam: PF00300; PGAM; 1.
CC KW Hypothetical protein.
SQ SEQUENCE 271 AA; 31022 MW; FF934DE2F5145C40 CRC64;
Query Match 72.5%; Score 37; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YGDYEG 7
DB 102 YGDYEG 107
RESULT 8
ASSY_METAC
ID ASSY_METAC STANDARD; PRT; 394 AA.
AC Q8TN5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
DE ligase).
GN ARG OR MA2142.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
CC -1- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
CC diphosphate + L-argininosuccinate.
CC -1- PATHWAY: Arginine biosynthesis; penultimate step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
CC
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CC -----
DR EMBL: AE010900; AAM05540.1;
DR PROSITE: PS00564; ARGININOSUCCIN_SYN_1; 1.
DR PROSITE: PS00565; ARGININOSUCCIN_SYN_2; 1.
KW Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SQ SEQUENCE 394 AA; 43994 MW; 2B995B9C138E7EF1 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 394;
Best Local Similarity 100.08; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDYEGY 8
Db 81 GDYEGY 86

RESULT 9
LHX5_BRARE
ID LHX5_BRARE STANDARD; PRT; 399 AA.
AC P52889;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5).
GN LHX5 OR LIM5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95377545; PubMed=7649385;
RA Toyama R., Curtiss P.E., Ocani H., Kimura M., David I.B., Taira M.;
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in
RT xenopus and zebrafish.";
RL Dev. Biol. 170:583-593(1995).
CC -!- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS
CC SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
CC DIENCEPHALON.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC -----
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CC -----
DR EMBL: L42547; AAA99465.1;
DR HSP: P06601; 1FJL.
DR ZFIN: ZDB-GENE-980526-484; lim5.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR001781; LIM.
DR Pfam: PF00046; homeobox; 1.
DR Pfam: PF00412; LIM; 2.
DR ProDom: PD000010; Homeobox; 1.
DR ProDom: PD000094; LIM; 2.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00132; LIM; 2.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS50023; LIM_DOMAIN_2; 2.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61
FT DOMAIN 62 125
FT DOMAIN LIM 1.
FT DOMAIN LIM 2.

FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 399 AA; 44513 MW; COD7BB1B86D032DA CRC64;

Query Match 72.5%; Score 37; DB 1; Length 399;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGDYEG 7
Db 278 YGEYQG 284

RESULT 10
SOX8_HUMAN
ID SOX8_HUMAN STANDARD; PRT; 446 AA.
AC P57073; Q9NZW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor SOX-8.
GN SOX8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Cheng Y.-C., Badge R.M., Armour J.A.L., Scotting P.J.;
RT "SOX8: a newly identified human gene expressed in paediatric brain
RT tumours and a candidate for the mental retardation phenotype in
RT ATR-16.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Ellington A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 119-446 FROM N.A.
RX MEDLINE=20130119; PubMed=10662550;
RA Pfeiffer D., Poulat F., Holinski-Feder E., Kooy F., Scherer G.;
RT "The SOX8 gene is located within 700 kb of the tip of chromosome 16p
RT and is deleted in a patient with ATR-16 syndrome.";
RL Genomics 63:108-116(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN CENTRAL NERVOUS SYSTEM, LIMB AND
CC FACIAL DEVELOPMENT. MAY BE INVOLVED IN MALE SEX DETERMINATION.
CC BINDS THE CONSENSUS MOTIF 5'-(AT)[AT]CAA[AT]G-3' (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: CONTAINS 1 HMG BOX.
CC -----
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CC -----
DR EMBL: AF226675; AAF35886.1;
DR EMBL: AF006465; AAK61260.1;
DR EMBL: Z99757; CAB75612.1; ALT_INIT.
DR EMBL: AF164104; AAF37424.1;
DR HSP: P48436; ISX9.
DR TRANSFAC: T04917;
DR Genew; HGNC:11203; SOX8.
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DR MIM: 605923;
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF00505; HMG_box_1.
DR SMART: SM00398; HMG; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 102 170 HMG_BOX.
SQ SEQUENCE 446 AA; 47314 MW; AE453359051A6DB3 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 446;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YGDIYEGY 8
||| |||
Db 391 YGAVPGY 398

RESULT 11

ROR_HUMAN STANDARD; PRT; 633 AA.
AC O43390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein R (hnRNP R).
GN HNRNP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98083170; PubMed=9421497;
RA Hassfeldt W., Chan E.K.L., Mathison D.A., Portman D., Dreyfuss G.,
RA Steiner G., Tan E.M.;
RT "Molecular definition of heterogeneous nuclear ribonucleoprotein R
(hnRNP R) using autoimmune antibody: Immunological relationship with
hnRNP P";
RL Nucleic Acids Res. 26:439-445(1998).
CC -1- FUNCTION: COMPONENT OF RIBONUCLEOSOMES, WHICH ARE COMPLEXES OF AT
CC LEAST 20 OTHER DIFFERENT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS
(HNRNP). HNRNP PLAY AN IMPORTANT ROLE IN PROCESSING OF PRECURSOR
CC MRNA IN THE NUCLEUS.
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
CC -1- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
CC
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CC
CC EMBL: AF000364; AAC39540.1;
CC HSP; P09651; 1HA1.
CC Genew: HGNC:5047; HNRNP.
CC InterPro: IPR000504; RNA_rec_mot.
CC Pfam: PF00076; rrm; 3
CC SMART: SM00360; RRM; 3.
CC PROSITE: PS0102; RRM; 3.
CC PROSITE: PS00030; RRM_RNP_1; 2.
KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.
FT DOMAIN 1 153 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 412 418 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 165 244 RNA-BINDING (RRM) 1.
FT DOMAIN 246 328 RNA-BINDING (RRM) 2.
FT DOMAIN 341 411 RNA-BINDING (RRM) 3.
FT DOMAIN 447 567 RNA-BINDING (RGG-BOX).
FT DOMAIN 462 497 3 X 11 AA APPROXIMATE REPEATS OF D-D-Y-Y-
FT G-Y-D-Y-H-D-Y.
FT REPEAT 462 471 1 (APPROXIMATE).
FT REPEAT 472 482 2.

FT REPEAT 488 497 3 (APPROXIMATE).
FT DOMAIN 579 633 GLN/ASN-RICH DOMAIN
SQ SEQUENCE 633 AA; 70943 MW; 088341F6465ED46F CRC64;

Query Match 72.5%; Score 37; DB 1; Length 633;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YGDIYEGY 8
||| |||
Db 470 YDDIYGY 477

RESULT 12

GL3A_DICDI STANDARD; PRT; 730 AA.
AC P34115;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cell surface glycoprotein GPI38A precursor.
GN FUSA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-32.
RC STRAIN=AX3;
RX MEDLINE=93193972; PubMed=7680629;
RA Fang H., Higa M., Suzuki K., Alba K., Urushihara H., Yanagisawa K.;
RT "Molecular cloning and characterization of two genes encoding gp138,
a cell surface glycoprotein involved in the sexual cell fusion of
Dictyostelium discoideum";
RL Dev. Biol. 156:201-208(1993).
CC -1- FUNCTION: INVOLVED IN THE SEXUAL CELL FUSION OF D.DISCOIDEUM.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
CC THAT CONTAINS A PHOSPHOCERAMIDE MOIETY.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT THE TIME OF ACQUISITION OF
CC FUSION COMPETENCE OF CELLS.
CC -1- PTM: THE SUGAR CHAINS MAY PLAY IMPORTANT ROLES IN CELL FUSION.
CC -1- MISCELLANEOUS: GPI38A EXPRESSION IS MUCH HIGHER THAN THAT OF
CC GPI38B AND MAY WELL BE THE MAJOR GENE FOR GPI38 PRODUCT.
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CC
CC EMBL: D12883; BAA02287.1;
CC PIR: A48832; A48832.
CC Dictydb; DD03014; fusa.
CC InterPro: IPR002909; IPT_TIG.
CC Pfam: PF01833; TIG; 1.
KW Glycoprotein; Signal; Multigene family; GPI-anchor; Repeat.
FT SIGNAL 1 20
FT CHAIN 21 708 CELL SURFACE GLYCOPROTEIN GPI38A.
FT PROPEP 709 730 REMOVED IN MATURE FORM (POTENTIAL).
FT LIPID 708 708 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 683 694 3 X 4 AA TANDEM REPEATS OF P-S-T-T.
FT REPEAT 683 686 1.
FT REPEAT 687 690 2.
FT REPEAT 691 694 3.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 596 596 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 605 605 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 730 AA; 80960 MW; C2BDB82BC24CD133 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 730;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YGDYEGY 8
||| |||
Db 343 YNDYEQY 350

RESULT 13
GGT_BACSU
ID GGT_BACSU STANDARD; PRT; 587 AA.
AC P54422;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2).
GN GGT.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=96312380; PubMed=8763966;
RA Xu K., Strauch M.A.;
RT "Identification, sequence, and expression of the gene encoding gamma-
RL glutamyltranspeptidase in Bacillus subtilis.";
RN J. Bacteriol. 178:4319-4322(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabet C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halesch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

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RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RT Nature 390:249-256(1997).
[3]
RN SEQUENCE OF 36-52 AND 403-442, AND CHARACTERIZATION.
RC STRAIN=NR-1;
RA Ogawa Y., Hosoyama H., Hamano M., Motai H.;
RT "Purification and properties of gamma-glutamyltranspeptidase from
RT Bacillus subtilis (natto).";
RL Agric. Biol. Chem. 55:2971-2977(1991).
CC -1- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid =
CC peptide + 5-L-glutamyl-amino acid.
CC -1- ENZYME REGULATION: INHIBITED BY GLUCOSE.
CC -1- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A
CC PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.
CC -1- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE
CC SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF VEGETATIVE GROWTH.
CC -1- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
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CC EMBL; U49358; AAC44233.1; -.
CC DR EMBL; Z99113; CAB13724.1; -.
CC DR EMBL; Z99114; CAB13734.1; -.
CC DR MEROPS; T03.001; -.
CC DR Subtilist; BG1838; ggt.
CC DR InterPro; IPR000101; Gglutrnspptdase.
CC DR Pfam; PF01019; G_glu_transpept; 1.
CC DR PRINTS; PR01210; GGTRANSPASE.
CC DR TIGRFS; TIGR00066; g_glu_trans; 1.
CC PROSITE; PS00462; G_GLU_TRANSPPEPTIDASE; 1.
KW Transferrase; Acyltransferase; Signal; Glutathione biosynthesis;
KW Zymogen; Complete proteome.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 402 GAMMA-GLUTAMYLTRANSPPEPTIDASE LARGE CHAIN.
FT CHAIN 403 587 GAMMA-GLUTAMYLTRANSPPEPTIDASE SMALL CHAIN.
FT BINDING 467 467 GAMMA-GLUTAMYL (POTENTIAL).
FT CONFLICT 46 46 D -> V (IN REF. 3).
SQ SEQUENCE 587 AA; 64189 MW; 6BF200CBA882C4F6 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 587;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 YGDYEGY 8
: ||| :
Db 277 WGDYQGY 283

RESULT 14
ACSA_RHOCA
ID ACSA_RHOCA STANDARD; PRT; 656 AA.
AC O68040;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
DE activating enzyme).
GN ACS.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-SB1003 / St Louis;
RX MEDLINE=97404404; PubMed=9256491;
RA Vicek C., Faces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.;
RT "Sequence of a 189-kb segment of the chromosome of Rhodobacter
capsulatus SB1003."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
CC -1- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
acetyl-CoA.
CC -1- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF040496; AAC16126.1; -
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding.1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING.1.
KW Ligase.
SQ SEQUENCE: 656 AA; 72703 MW; 706EA969331D71C2 CRC64;

Query Match: 70.6%; Score 36; DB 1; Length 656;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
Db 495 YFGGIRCI 502

RESULT 15
PERT_MOUSE 1
ID PERT_MOUSE STANDARD; PRT; 914 AA.
AC P35419; 1
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thyroid peroxidase precursor (EC 1.11.1.8) (TPO).
GN TPO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=657BL/6; TISSUE=Thyroid;
RX MEDLINE=93154601; PubMed=7916704;
RA Kotani T., Umeki K., Yamamoto I., Takeuchi M., Takechi S.,
RA Nakayama T., Ohtaki S.;
RT "Nucleotide sequence of the cDNA encoding mouse thyroid peroxidase.";
RL Gene 128:289-290(1993).
CC -1- FUNCTION: IODINATION AND COUPLING OF THE HORMONOGENIC TYROSINES
CC IN THYROGLOBULIN TO YIELD THE THYROID HORMONES T(3) AND T(4).
CC -1- CATALYTIC ACTIVITY: Iodide + H(2)O(2) = iodine + 2 H(2)O.
CC -1- COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.
CC -1- PATHWAY: Thyroid hormone biosynthesis.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. XPO SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC
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CC
CC EMBL: X60703; CAA43114.1; -
DR PIR: JN0550; JN0550.
DR HSSP: P05164; LCXP.
DR MGD: MGI:98813; TPO.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR00152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002016; Peroxidase.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00008; EGF.1.
DR Pfam: PF00084; sushi.1.
DR Pfam: PF03098; An_peroxidase.1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR SMART: SM00032; CCP.1.
DR SMART: SM00179; EGF_Ca.1.
DR PROSITE: PS00010; ASX_HYDROXYL.1.
DR PROSITE: PS00435; PEROXIDASE_1.1.
DR PROSITE: PS01186; EGF.2.1.
DR PROSITE: PS01187; EGF_Ca.1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Transmembrane; Glycoprotein;
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 914 THYROID PEROXIDASE.
FT ACT_SITE 233 233 DISTAL HISTIDINE (POTENTIAL).
FT ACT_SITE 384 384 DISTAL ARGININE (POTENTIAL).
FT METAL 482 482 IRON (PROTOHEME IX AXIAL LIGAND) (BY
SIMILARITY).
FT TRANSMEM 835 859 POTENTIAL.
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 914 AA; 101342 MW; 595E9A0B71F3DD01 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 914;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
Db 454 YVGPYEGY 461

Search completed: December 23, 2002, 07:26:05
Job time : 3.7907 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 3.31783 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-3

Perfect score: 51

Sequence: 1 YGDYEGY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	80.4	435	Q9PN04	Q9pn04 campylobact
2	40	78.4	409	Q9LEB4	Q9leb4 nicotiana p
3	40	78.4	1650	5 O77328	O77328 plasmodium
4	39	76.5	1881	Q8TJS7	Q8tjs7 methanosarc
5	38	74.5	387	10 Q9FPJ8	Q9fpj8 arabidopsis
6	38	74.5	390	10 Q9FFU0	Q9ffu0 arabidopsis
7	38	74.5	595	16 Q67245	Q67245 aquifex aeo
8	38	74.5	660	16 Q9KGR8	Q9kg8 bacillus ha
9	38	74.5	3216	16 Q98QZ9	Q98qz9 mycoplasma
10	37	72.5	89	5 Q62093	Q62093 caenorhabdi
11	37	72.5	104	5 Q9UG01	Q9ug01 anisakis si
12	37	72.5	154	17 Q27163	Q27163 methanobact
13	37	72.5	248	5 Q9W0H1	Q9w0h1 drosophila
14	37	72.5	279	4 Q9HAF2	Q9haf2 homo sapien
15	37	72.5	294	2 Q8VWN1	Q8vwn1 vibrio chol
16	37	72.5	300	5 Q9W098	Q9w098 drosophila

17	37	72.5	376	4	Q9H7I9	Q9h7i9 homo sapien
18	37	72.5	394	17	Q8TNY5	Q8tny5 methanosarc
19	37	72.5	542	16	Q9JZ89	Q9jz89 neisseria m
20	37	72.5	542	16	Q9JUB3	Q9jub3 neisseria m
21	37	72.5	564	5	Q23118	Q23118 caenorhabdi
22	37	72.5	601	11	Q99KG1	Q99kg1 mus musculu
23	37	72.5	620	17	Q96XC8	Q96xc8 sulfolobus
24	37	72.5	632	11	Q8VHM5	Q8vhm5 mus musculu
25	37	72.5	636	4	Q9BV64	Q9bv64 homo sapien
26	37	72.5	1657	5	P90761	P90761 caenorhabdi
27	36	70.6	191	16	Q92CQ8	Q92cq8 listeria in
28	36	70.6	191	16	Q8Y7X0	Q8y7x0 listeria mo
29	36	70.6	252	16	Q97SL3	Q97sl3 streptococ
30	36	70.6	299	17	Q8TL35	Q8tl35 methanosarc
31	36	70.6	307	5	Q9V5P1	Q9v5p1 drosophila
32	36	70.6	307	17	Q8TMD1	Q8tdm1 methanosarc
33	36	70.6	335	5	Q8SZN5	Q8szn5 drosophila
34	36	70.6	335	5	Q8SP0	Q8sy0 drosophila
35	36	70.6	441	10	Q9LX71	Q9lx71 arabidopsis
36	36	70.6	565	16	Q98RF4	Q98rf4 mycoplasma
37	36	70.6	605	17	Q8UI30	Q8ui30 pyrococcus
38	36	70.6	618	10	Q9LMD5	Q9lmd5 oryza sativ
39	36	70.6	666	2	Q9RIK7	Q9rik7 thermotoga
40	36	70.6	669	16	Q9XQV4	Q9xqv4 thermotoga
41	36	70.6	680	2	Q9RIK9	Q9rik9 thermotoga
42	36	70.6	686	5	Q96453	Q96453 anopheles s
43	36	70.6	687	5	Q96753	Q96753 anopheles g
44	36	70.6	694	2	Q9Z187	Q9z187 bacillus st
45	36	70.6	760	4	Q8TCI9	Q8tc19 homo sapien

ALIGNMENTS

RESULT 1

Q9PN04 ID Q9PN04 PRELIMINARY; PRT; 435 AA.
AC Q9PN04;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Hypothetical protein Cj1295.
GN Cj1295.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; ALI39078; CAB73722.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 435 AA; 49948 MW; 1DFD6DD270C0877 CRC64;

Query Match 80.4%; Score 41; DB 16; Length 435;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGDYEGY 8

Db 325 YGDYDGY 331

RESULT 2

Q9LEB4
ID Q9LEB4 PRELIMINARY; PRT; 409 AA.
AC Q9LEB4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RNA binding protein 45.
GN RBP45.
OS Nicotiana glumabaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20555308; PubMed=11105760;
RA Lorkovic J.J., Wiczorek Kirk D.A., Klahre U., Hemmings-Mieszcak M.,
RA Filipowicz W.;
RT "RBP45 and RBP47, two oligouridylylate-specific hnRNP-like proteins
interacting with poly(A)+ RNA in nuclei of plant cells.";
RL RNA 6:1610-1624(2000).
DR EMBL: AJ292767; CAC01237.1; -
DR HSSP: P11840; 1CVJ.
DR ANU-2DPAGE; Q9LEB4; -
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; RRM; 3.
DR SMART: SM00360; RRM; 3.
DR PROSITE: PS50102; RRM; 3.
DR PROSITE: PS00030; RRM_RNP.1; UNKNOWN.1.
SQ SEQUENCE 409 AA; 45243 MW; 145EE701A9AFA01D CRC64;

Query Match: 78.4%; Score 40; DB 10; Length 409;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDDYEGY 8
Db 394 YGNYPGY 401
| | | | | | | |

RESULT 3
O77328
ID O77328 PRELIMINARY; PRT; 1650 AA.
AC O77328
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative serine/threonine protein kinase.
GN PFC0385; MAL3P3.12.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagsels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares S., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum.";
RL Nature 400:532-538(1999).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Z98547; CAB11112.2; -
DR HSSP: Q63450; 1A06.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.

DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN.1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1650 AA; 193755 MW; D70FEL9C5C640B5A CRC64;

Query Match: 78.4%; Score 40; DB 5; Length 1650;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDDYEGY 8
Db 525 YFDDYEGY 532
| | | | | | | |

RESULT 4
Q8TJS7
ID Q8TJS7 PRELIMINARY; PRT; 1881 AA.
AC Q8TJS7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cell surface protein.
GN MA3700.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Ancoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL: AE011081; AAM07055.1; -
KW Complete proteome.
SQ SEQUENCE 1881 AA; 201366 MW; 836514E38E842A49 CRC64;

Query Match: 76.5%; Score 39; DB 17; Length 1881;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDDYEGY 8
Db 165 HXGDYGY 172
| | | | | | | |

RESULT 5
Q9FPJ8
ID Q9FPJ8 PRELIMINARY; PRT; 387 AA.
AC Q9FPJ8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AT5G54900.
GN AT5G54900/MBG8.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chao Q., Brooks S., Chen H., Cheuk R., Johnson-Hopson C.,
RA Khan S., Kim C.J., Banh J., Bowser L., Chung M.K., Goldsmith A.D.,
RA Jones T., Karlin-Neumann G., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H.,
RA Southwick A., Toriumi M., Yamada K., Yu G., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF324983; AAG40335.1; -.
DR HSSP; P11940; ICVJ.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 387 AA; 42324 MW; D6CF4F66DFD78DB0 CRC64;

Query Match 74.5%; Score 38; DB 10; Length 387;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
Db 372 YGGYTG 379

RESULT 6
Q9FFU0 PRELIMINARY; PRT; 390 AA.
AC Q9FFU0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similarity to polyadenylate-binding protein 5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AB052322; BAB08769.1; -.
DR HSSP; P11940; ICVJ.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 390 AA; 42652 MW; DD03B776CF4F66DF CRC64;

Query Match 74.5%; Score 38; DB 10; Length 390;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDIYEGY 8
Db 372 YGGYTG 379

RESULT 7
O67245 PRELIMINARY; PRT; 595 AA.
ID O67245

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AC O67245;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein AQ_1185.
GN AQ_1185.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000727; AAC07204.1; -.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 2.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 595 AA; 71080 MW; F8373F5603427F24 CRC64;

Query Match 74.5%; Score 38; DB 16; Length 595;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGDYEGY 8
Db 159 YGDTGY 165

RESULT 8
Q9KGK8 PRELIMINARY; PRT; 660 AA.
AC Q9KGK8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10).
OS METS OR BH0053.
OC Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001507; BAB03772.1; -.
DR HSSP; P23395; IAH8.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR Pfam; PF00133; tRNA_bind.
DR Pfam; PF01588; tRNA_bind; 1.
DR PRINTS; PR01041; TRNASYNTHMET.
DR TIGRFAMS; TIGR00398; metG; 1.
DR TIGRFAMS; TIGR00399; metG_C-term; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; UNKNOWN_1.
KW Aminoacyl-tRNA synthetase; Ligase; Complete proteome.
SQ SEQUENCE 660 AA; 75191 MW; EC3408645728A536 CRC64;

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Query Match 74.5%; Score 38; DB 16; Length 660;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDEYEGY 8
 ||| |||
 Db 121 YLGDYEGW 128

RESULT 9

Q98Q29 : PRELIMINARY; PRT; 3216 AA.
 AC Q98Q29;
 DT 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Hypothetical protein MYPU_2110.
 GN MYPU_2110.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis.";
 RL Nucleic Acids Res. 29:2145-2153(2001).
 DR EMBL; AL045563; CAC13384.1; -;
 DR MYPUList MYPU_2110; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 3216 AA; 359419 MW; A62ED95756BDB90C CRC64;

Query Match 74.5%; Score 38; DB 16; Length 3216;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGDEYEGY 8

||| |||
 Db 1978 YVDYEGF 1985

RESULT 10

O62093 : PRELIMINARY; PRT; 89 AA.
 AC O62093;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE C37A5.8 protein.
 GN C37A5.8
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA White S.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z92828; CAB07335.1; -;
 SQ SEQUENCE 89 AA; 10003 MW; C887044842E59E25 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 89;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDEYEGY 8
 ||| |||
 Db 61 YGGYGGY 68

RESULT 11

Q9U601 : PRELIMINARY; PRT; 104 AA.
 AC Q9U601;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Hypothetical 11.5 kDa protein.
 GN IAA99-ASL3-15A.
 OS Anisakis simplex.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Anisakidae; Anisakis.
 OX NCBI_TaxID=6269;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Arrieta I., Del Barrio M., Vidarte L., Del Pozo V., Pastor C.,
 RA Gonzalez-Cabrejo J., Cardaba B., Rojo M., Minguez A., Corteano I.,
 RA Gallardo S., Aceituno E., Palomino P., Lahoz C.;
 RT "Anisakis simplex for a 12 kDa protein.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ250043; CAB58174.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 11456 MW; 419710152ADD6FAA CRC64;

Query Match 72.5%; Score 37; DB 5; Length 104;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGDEYEGY 8
 ||| |||
 Db 63 YGGYGGY 70

RESULT 12

O27163 : PRELIMINARY; PRT; 154 AA.
 AC O27163;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Conserved protein.
 GN MTH1091.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer C., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT J. Bacteriol. 179:7135-7155(1997)."
 RL EMBL; AE000879; AAB85580.1; -;
 DR InterPro; IPR002743; DUF57.
 DR Pfam; PF01881; DUF57; 1.
 DR ProDom; PD008324; DUF57; 1.

KW Complete proteome.
SQ SEQUENCE 154 AA; 18541 MW; 9EA3B9F89F7DE210 CRC64;

Query Match 72.5%; Score 37; DB 17; Length 154;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGDIYEG 7
:||||:|
Db 81 FYGDIYDG 87

RESULT 13

Q9WOH1 PRELIMINARY; PRT; 248 AA.
AC Q9WOH1:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG9184 protein.
GN CG9184.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista A.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003471; AAF47476.1; -
DR FlyBase; FBgn0035208; CG9184.
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENS.
SQ SEQUENCE 248 AA; 26964 MW; 59CE24C83A55A3CD CRC64;

Query Match 72.5%; Score 37; DB 5; Length 248;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGDIYEG 8
:||||:|
Db 160 YGGYGGY 167

RESULT 14

Q9HAF2 PRELIMINARY; PRT; 279 AA.
AC Q9HAF2:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 30.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK021791; BAB13897.1; -
DR InterPro; IPR004567; Pank_eukar.
DR Pfam; PF03630; Fumble; 1.
SQ SEQUENCE 279 AA; 30651 MW; AAD5D4A2C94AEA3C CRC64;

Query Match 72.5%; Score 37; DB 4; Length 279;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGDIYEG 8
:||||:|
Db 163 YGGYEGF 170

RESULT 15

Q8VVN1 PRELIMINARY; PRT; 294 AA.
AC Q8VVN1:
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 33.0 kDa protein.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MO10; TRANSDON-SXT ELEMENT;
RX MEDLINE=21485931; PubMed=11600347;
RA Hochhut B., Lotfi Y., Mazel D., Faruque S.M., Woodgate R.,
RA Waldor M.K.;
RT "Molecular Analysis of Antibiotic Resistance Gene Clusters in Vibrio
cholerae O139 and O1 SXT Constsins."
RL Antimicrob. Agents Chemother. 45:2991-3000(2001).
DR EMBL; AY034138; AAK64586.1; -
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 33023 MW; A0A2FA4C0173018F CRC64;

Query Match 72.5%; Score 37; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GDYEGY 8
|||||
Db 74 GDYEGY 79

Search completed: December 23, 2002, 07:29:47
Job time : 6.31783 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 5.36822 seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-4
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Sequence: 1 SASSSVSVMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
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1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*		
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*		
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*		
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*		
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*		
6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*		
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*		
8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*		
9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*		
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*		
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*		
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*		
13:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*		
14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*		
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*		
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*		
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*		
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*		
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*		
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*		
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*		
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*		
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	10	AAW27424	CDR1 from light ch
2	48	100.0	10	AAW73169	CDR1 of light chai
3	48	100.0	10	AAW28390	Peptide fragment f
4	48	100.0	10	AAW97232	Complementary dete
5	48	100.0	10	AAW77582	Anti-human VEGF re
6	48	100.0	10	AAW77588	Anti-human VEGF re
7	48	100.0	10	AAE13140	Humanised antibody
8	48	100.0	10	AAW82706	VEGF antagonist an
9	48	100.0	10	AAW83163	Mouse ganglioside
10	48	100.0	10	AAW78851	Anti-human Fit-1 a

11	48	100.0	10	22	AAW78857	Anti-human Fit-1 a
12	48	100.0	10	23	AAU74409	Light chain comple
13	48	100.0	10	23	AAU70361	Mouse Kappa VI lig
14	48	100.0	96	22	AAU08982	Single-chain antib
15	48	100.0	99	22	AAU08981	Single-chain antib
16	48	100.0	102	11	AAU07321	VK domain of antib
17	48	100.0	102	17	AAW14489	Monoclonal antibod
18	48	100.0	102	17	AAW99872	Monoclonal antibod
19	48	100.0	103	13	AAW26002	L-chain variable r
20	48	100.0	105	17	AAW03182	Guy's 13 anti-Stre
21	48	100.0	106	22	AAE13144	Humanised antibody
22	48	100.0	106	23	AAU74418	Antigen-binding pr
23	48	100.0	107	22	AAW83159	Mouse ganglioside
24	48	100.0	107	22	AAW83167	Ganglioside GM2 an
25	48	100.0	108	13	AAW21293	Murine VL kappa gr
26	48	100.0	108	13	AAW21301	Murine VL kappa gr
27	48	100.0	108	13	AAW21303	Murine VL kappa gr
28	48	100.0	108	16	AAW79884	Anti-EGFR antibody
29	48	100.0	108	21	AAW97236	Variable light cha
30	48	100.0	108	22	AAW82710	VEGF antagonist an
31	48	100.0	108	23	AAU74413	Antigen-binding pr
32	48	100.0	110	18	AAW21846	Light chain variab
33	48	100.0	113	22	AAW48936	Anti-trkA murine m
34	48	100.0	125	22	AAE13146	Chimeric pIC11 lig
35	48	100.0	125	22	AAW82702	VEGF antagonist an
36	48	100.0	126	21	AAW77594	Anti-human VEGF re
37	48	100.0	126	21	AAW77598	Anti-human VEGF re
38	48	100.0	126	21	AAW77599	Anti-human VEGF re
39	48	100.0	126	21	AAW77601	Anti-human VEGF re
40	48	100.0	126	22	AAW78863	Anti-human Fit-1 m
41	48	100.0	126	22	AAW78867	Anti-human Fit-1 a
42	48	100.0	126	22	AAW78868	Anti-human Fit-1 a
43	48	100.0	126	22	AAW78870	Anti-human Fit-1 a
44	48	100.0	128	21	AAW77592	Anti-human VEGF re
45	48	100.0	128	21	AAW77597	Anti-human VEGF re

ALIGNMENTS

RESULT 1	
AAW27424	
ID	AAW27424 standard; peptide; 10 AA.
XX	
AC	AAW27424;
XX	
DT	19-DEC-1997 (first entry)
XX	
DE	CDR1 from light chain variable region of KM1486 antibody.
XX	
KW	Complementarity determining region; CDR; light chain; treatment;
KW	variable region; murine; mouse; human; interleukin 5; IL-5;
KW	receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW	assay; diagnosis; allergic respiratory disease; chronic bronchitis;
XX	
OS	Mus spp.
XX	
PN	WO9710354-A1.
XX	
PD	20-MAR-1997.
XX	
PF	11-SEP-1996; 96WO-JP02588.
XX	
PR	11-SEP-1995; 95JP-0232384.
XX	
PA	(KYOW) KYOWA HAKKO KOGYO KK.
XX	
PI	Anazawa H, Furuya A, Hanai N, Iida A, Koike M;
PI	Nakamura K, Takatsu K;
XX	
DR	WPI; 1997-202249/18.
XX	
PT	Antibody against alpha-chain of human interleukin 5 receptor -

PT useful for diagnosis and treatment of respiratory allergic diseases,
 PT e.g. chronic bronchitis

PS Claim 10; Page 165; 238pp; Japanese.

XX The present sequence is complementarity determining region 1 (CDR1)
 CC from the light chain variable region of the murine anti-human
 CC interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal
 CC antibody (MAB) KM1486. KM1486 is produced by the hybridoma
 CC FERM BP-5851, which was prepared by immunising Balb/c mice with
 CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
 CC myeloma PG-U1 cells and screening the resultant hybridomas. The MAB
 CC can be used to detect or assay for hIL-5R alpha and cells
 CC expressing it on their surface, especially to diagnose allergic
 CC respiratory diseases, e.g. chronic bronchitis. It can also be used
 CC to treat such diseases.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 18; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 1 SASSSVSVMH 10

RESULT 2

AAW73169

ID AAW73169 standard; peptide; 10 AA.

AC AAW73169;

XX

DT 22-JAN-1999 (first entry)

DE

XX CDR1 of light chain of ganglioside GM2 targeting antibody.

XX Ganglioside GM2; antibody; complementarity determining region; cancer;
 KW anti-tumour agent.

XX Homo sapiens.

XX JP10257893-A.

XX 29-SEP-1998.

XX 19-MAR-1997; 97JP-0056981.

XX 19-MAR-1997; 97JP-0056981.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX WPI; 1998-575904/49.

PT A human type complementarity determining region transplanted
 PT antibody against ganglioside GM2 - useful as an anti-tumour agent
 PT and as a diagnostic for related cancers

PS Claim 1; Page 29; 66pp; Japanese.

XX This sequence represents a complementarity determining region (CDR) from
 CC the heavy chain of the antibody of the invention. The antibody of the
 CC invention is a human CDR transplanted antibody that reacts specifically
 CC with ganglioside GM2. DNA encoding the antibody, and vectors and
 CC transformants containing it, can be used for the recombinant production
 CC of the antibody. The antibody itself can be used as an anti-tumour agent
 CC or as a diagnostic tool for related cancers. The antibody has antitumour
 CC activity against ganglioside GM2 positive cells.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 1 SASSSVSVMH 10

RESULT 3

AAI28390

ID AAY28390 standard; Protein; 10 AA.

AC AAY28390;

XX

DT 04-NOV-1999 (first entry)

DE

XX Peptide fragment from the human anti-GM2 light chain in REI.

XX antibody; REI; complementarity determining region; CDR;

KW chimeric; light chain; heavy chain.

XX Homo sapiens.

XX US5939532-A.

XX 17-AUG-1999.

XX 07-JUN-1995; 95US-0483528.

XX 07-JUN-1995; 95US-0483528.

XX 07-SEP-1993; 93US-0116778.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;

XX Shitara K;

XX WPI; 1999-468416/39.

XX Chimeric human antibody expression vectors

XX Example 2; Column 157; 188pp; English.

XX The sequences AAY28390 to AAY28392 replace the CDR regions of the NEWM
 CC DNA and they produce AAY28394, the hKM796L human anti-GM2 antibody light
 CC chain.
 CC Chimeric human antibodies of the invention are useful in the treatment
 CC of cancer, especially that which is of neural ectodermal origin.
 CC In contrast to prior art constructs based on mouse monoclonal
 CC antibodies, the chimeric human antibodies do not cause anti-mouse
 CC immunoglobulin production.
 CC The chimeric human antibodies have a prolonged half-life and a reduced
 CC frequency of adverse effects when compared to mouse monoclonal
 CC antibodies.

XX Sequence 10 AA;

Query Match 100.0%; Score 48; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 1 SASSSVSVMH 10

RESULT 4

AAI97232

ID AAY97232 standard; Protein; 10 AA.

XX

AC AAY97232;

XX

DT 19-DEC-2000 (first entry)

The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region

The present sequence is that of complementarity determining region 1 of the light chain variable region (see also AAB92702) of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent to produce

CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The anti-angiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
 XX Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
 |||||
 Db 1 SASSSSVSYMH 10

RESULT 9

AAB83163
 ID AAB83163 standard; peptide; 10 AA.

AC AAB83163;

DT 02-JUL-2001 (first entry)

XX Mouse ganglioside GM2 antibody light chain variable region CDR1.
 DE Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer;
 KW complementarity determining region; CDR.
 XX

OS Mus sp.

XX WO200123431-A1.

PN 05-APR-2001.

PD 29-SEP-2000; 2000WO-JP06775.

PF 30-SEP-1999; 99JP-0278292.

PR (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Nakamura K, Niwa R;

PI WPI; 2001-266142/27.

XX Monoclonal antibodies against ganglioside GM2 combined with drugs,
 PT radioisotopes or proteins for treatment and diagnosis of cancer -
 PT

PS Claim 4; Page 71; 80pp; Japanese.

XX The present invention relates to derivatives of an antibody against
 CC ganglioside GM2. The antibody may be a monoclonal antibody or its
 CC fragments. The antibody is combined with a radioactive isotope,
 CC protein or small drug in the treatment and diagnosis of cancer.
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
 |||||
 Db 1 SASSSSVSYMH 10

RESULT 10

DE Anti-human Flt-1 antibody KM1750 L chain V region CDR 1 peptide.

AAB78851

ID AAB78851 standard; Peptide; 10 AA.

XX AAB78851;

XX 20-APR-2001 (first entry)

DE Anti-human Flt-1 antibody KM1732 L chain V region CDR 1 peptide.

XX Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
 KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
 KW delayed hypersensitivity; malignant tumour; arteriosclerosis.
 XX

OS Mus musculus.

PN WO200079275-A1.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-JP03957.

XX 17-JUN-1999; 99JP-0171709.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Shibuya M;

XX WPI; 2001-080847/09.

XX Substances binding to human vascular endothelial growth factor receptor
 Flt-1, used for diagnosis and treatment of inflammatory diseases,
 PT arteriosclerosis, cancer and delayed hypersensitivity -
 PT

PS Example 3; Page 127; 164pp; Japanese.

XX This invention relates to a reagent for detecting differentiation of
 CC monocytes and macrophages from haematopoietic stem cells, containing a
 CC substance which binds to human vascular endothelial growth factor (VEGF)
 CC receptor Flt-1. The invention also includes a method for diagnosing a
 CC disease in which the differentiation of monocytes and macrophages is
 CC implicated, using the reagent, and an agent for the treatment of diseases
 CC diagnosed using the method, containing a substance which binds to Flt-1
 CC or a substance which inhibits the signal transduction of Flt-1. Diseases
 CC which may be diagnosed or treated include inflammation, delayed
 CC hypersensitivity, malignant tumours and arteriosclerosis.
 CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences
 CC encoding anti-human Flt-1 monoclonal antibody fragments, and
 CC oligonucleotides used in the construction of the antibody. The monoclonal
 CC antibody is used in the reagent of the invention. PCR primers AAF70245 -
 CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody
 CC DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments
 CC of the anti-human Flt-1 antibody.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSSVSYMH 10
 |||||
 Db 1 SASSSSVSYMH 10

RESULT 11

AAB78857
 ID AAB78857 standard; peptide; 10 AA.

XX AAB78857;

XX 20-APR-2001 (first entry)

DE Anti-human Flt-1 antibody KM1750 L chain V region CDR 1 peptide.

XX Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
 KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
 KW delayed hypersensitivity; malignant tumour; arteriosclerosis.
 XX
 OS Mus musculus.
 PN WO200079275-A1.
 XX
 PD 28-DEC-2000.
 XX
 XX 16-JUN-2000; 2000WO-JP03957.
 PF
 XX 17-JUN-1999; 99JP-0171709.
 PR
 XX (KYOWA) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Shibuya M;
 PI
 XX WPI; 2001-080847/09.
 DR
 XX Substances binding to human vascular endothelial growth factor receptor
 PT Flt-1, used for diagnosis and treatment of inflammatory diseases,
 PT arteriosclerosis, cancer and delayed hypersensitivity -
 XX
 PS Example 3; Page 128; 164pp; Japanese.
 XX
 CC This invention relates to a reagent for detecting differentiation of
 CC monocytes and macrophages from haematopoietic stem cells, containing a
 CC substance which binds to human vascular endothelial growth factor (VEGF)
 CC receptor, Flt-1. The invention also includes a method for diagnosing a
 CC disease in which the differentiation of monocytes and macrophages is
 CC implicated, using the reagent, and an agent for the treatment of diseases
 CC diagnosed using the method, containing a substance which binds to Flt-1
 CC or a substance which inhibits the signal transduction of Flt-1. Diseases
 CC which may be diagnosed or treated include inflammation, delayed
 CC hypersensitivity, malignant tumours and arteriosclerosis.
 CC AAF701907 - AAF70244, AAF70251 and AAF70258 represent DNA sequences
 CC encoding anti-human Flt-1 monoclonal antibody fragments, and
 CC oligonucleotides used in the construction of the antibody. The monoclonal
 CC antibody is used in the reagent of the invention. PCR primers AAF70245 -
 CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody
 CC DNA sequences. Protein sequences AAF78848 - AAF78870 represent fragments
 CC of the anti-human Flt-1 antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 48; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SASSSVSYMH 10
 Db |||||
 1 SASSSVSYMH 10
 RESULT 12
 AAU74409
 ID AAU74409 standard; peptide; 10 AA.
 XX
 AC AAU74409;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Light chain complementarity determining region L1 (CDRL1).
 DE
 XX Complementarity determining region; CDR; CDRL1; antigen; cytostatic;
 KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
 KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
 KW antibody light chain variable domain.
 XX
 OS Mus sp.
 XX

PN WO200190192-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US16924.
 XX
 PR 24-MAY-2000; 2000US-206749P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Zhu Z;
 XX
 XX WPI; 2002-106189/14.
 DR
 DR N-PSDB; AAS20280.
 XX
 XX New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides -
 XX
 PS Claim 55; Page 56; 64pp; English.
 XX
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an Ig molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This peptide sequence represents the light chain variable domain
 CC complementarity determining region L1 (CDRL1) incorporated into an
 CC antigen-binding protein described in the method of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 48; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SASSSVSYMH 10
 Db |||||
 1 SASSSVSYMH 10
 RESULT 13
 AAU70361
 ID AAU70361 standard; Peptide; 10 AA.
 XX
 AC AAU70361;
 XX
 XX 14-FEB-2002 (first entry)
 DT
 XX Mouse Kappa VI light chain CDRL1.
 DE
 XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX
 OS Mus musculus.
 XX
 PN WO200183806-A1.

XX 08-NOV-2001.
 XX
 XX
 XX 02-MAY-2001; 2001WO-US14349.
 XX
 XX 02-MAY-2000; 2000US-0563222.
 XX
 XX (EPIC-) EPICYTE PHARM INC.
 XX
 XX Hiatt AC, Hein MB;
 XX
 XX WPI; 2002-055482/07.
 XX
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -
 XX
 XX Disclosure; Page 14; 129pp; English.
 XX
 XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgE, IgI, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells, especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 48; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SASSSVSVMH 10
 DB 1 SASSSVSVMH 10
 |||||
 RESULT 14
 AAU08982
 ID AAU08982 standard; protein; 96 AA.
 XX
 AC AAU08982;
 XX
 XX 18-DEC-2001 (first entry)
 XX
 XX Single-chain antibody scFvA7 light chain.
 DE
 XX Antibody; scFvA7; light chain; angiogenesis; vascularisation;
 KW vascular endothelial; growth factor receptor 2; VEGFR-2; carcinoma.
 XX
 XX Mus sp.
 OS Synthetic.
 XX
 XX EP1130032-Al.
 PN
 XX 05-SEP-2001.
 PD
 XX 28-FEB-2000; 2000EP-0104082.
 PF
 XX 28-FEB-2000; 2000EP-0104082.
 XX
 XX

PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 XX
 XX Boeldicke T, Weich H, Tesar M, Yayon A;
 XX
 XX WPI; 2001-591521/67.
 DR
 XX
 XX Single-chain antibody that recognizes human vascular endothelial growth
 PT factor receptor-2 is useful as a marker for angiogenesis or
 PT vascularisation in human tissues and for cell sorting of vascular
 PT endothelial cells -
 XX
 XX Claim 1; Page 20; 35pp; English.
 XX
 XX The invention relates to novel single-chain antibody recognizing human
 CC vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a
 CC polypeptide having variable heavy (VH) and variable light (VL) domains
 CC connected by a linker, and their allelic variants and mutants. The
 CC antibody is useful as an immunohistochemical marker for angiogenesis
 CC or vascularisation in a human tissue from cryosection or a growing
 CC carcinoma, for vascular and stem cell targeting a drug or toxin,
 CC radionuclide, gene or viral coat protein conjugated to it, for
 CC fluorescence activated cell sorting (FACS) analysis and sorting of
 CC cells expressing human vascular endothelial growth factor receptor-2,
 CC such as human vascular endothelial cells, human megakaryocytes and
 CC their progenitor cells, human haematopoietic stem cells from bone
 CC marrow, umbilical cord blood or mobilised peripheral blood on their
 CC surfaces. Recombinant single chain antibodies have many advantages
 CC compared to monoclonal antibodies derived from hybridomas. The
 CC recombinant antibodies are more easily expressed and prepared in
 CC bacteria, easily purified from the bacteria periplasm or supernatant
 CC without risk of contamination with serum-components. No expensive
 CC cell-culture medium and expensive cell-culture laboratory is needed and
 CC they are prepared by economical and cheap method. Because of the small
 CC size they penetrate better into cells and tissue and are better used
 CC for in vivo imaging and in vivo diagnostic applications. The
 CC single-chain antibodies are easily fused to a drug, toxin,
 CC radionuclide, gene or a viral coat protein. The present sequence is
 CC the variable light chain of antibody scFvA7.
 XX
 XX Sequence 96 AA;
 SQ
 Query Match 100.0%; Score 48; DB 22; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SASSSVSVMH 10
 DB 16 SASSSVSVMH 25
 |||||
 RESULT 15
 AAU08981
 ID AAU08981 standard; protein; 99 AA.
 XX
 AC AAU08981;
 XX
 XX 18-DEC-2001 (first entry)
 XX
 XX Single-chain antibody scFvA2 light chain.
 DE
 XX Antibody; scFvA7; light chain; angiogenesis; vascularisation;
 KW vascular endothelial; growth factor receptor 2; VEGFR-2; carcinoma.
 XX
 XX Mus sp.
 OS Synthetic.
 XX
 XX EP1130032-Al.
 PN
 XX 05-SEP-2001.
 PD
 XX 28-FEB-2000; 2000EP-0104082.
 PF
 XX 28-FEB-2000; 2000EP-0104082.
 XX
 XX

XX (GBFE) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PA Boeldicke T, Weich H, Tesar M, Yayon A;
 PI WPI; 2001:591521/67.
 XX
 XX Single-chain antibody that recognizes human vascular endothelial growth
 PT factor receptor-2 is useful as a marker for angiogenesis or
 PT vascularisation in human tissues and for cell sorting of vascular
 PT endothelial cells
 XX
 PS Claim 1; Page 20; 35pp; English.
 XX
 CC The invention relates to novel single-chain antibody recognizing human
 CC vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a
 CC polypeptide having variable heavy (VH) and variable light (VL) domains
 CC connected by a linker, and their allelic variants and mutants. The
 CC antibody is useful as an immunohistochemical marker for angiogenesis
 CC or vascularisation in a human tissue from cryosection or a growing
 CC carcinoma, for vascular and stem cell targeting a drug or toxin,
 CC radionuclide, gene or viral coat protein conjugated to it, for
 CC fluorescence activated cell sorting (FACS) analysis and sorting of
 CC cells expressing human vascular endothelial growth factor receptor-2,
 CC such as human vascular endothelial cells, human megakaryocytes and
 CC their progenitor cells, human haematopoietic stem cells from bone
 CC marrow, umbilical cord blood or mobilised peripheral blood on their
 CC surfaces. Recombinant single chain antibodies have many advantages
 CC compared to monoclonal antibodies derived from hybridomas. The
 CC recombinant antibodies are more easily expressed and prepared in
 CC bacteria easily purified from the bacteria periplasm or supernatant
 CC without risk of contamination with serum-components. No expensive
 CC cell-culture medium and expensive cell-culture laboratory is needed and
 CC they are prepared by economical and cheap method. Because of the small
 CC size they penetrate better into cells and tissue and are better used
 CC for in vivo imaging and in vivo diagnostic applications. The
 CC single-chain antibodies are easily fused to a drug, toxin,
 CC radionuclide, gene or a viral coat protein. The present sequence is
 CC the variable light chain of antibody scFvA2.
 XX

SQ Sequence 99 AA;

Query Match 100.0%; Score 48; DB 22; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSSVSYMH 10
 Db 16 SASSSSVSYMH 25

Search completed: December 23, 2002, 07:25:05
 Job time : 6136822 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 0.930233 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSVMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	48	100.0	10	10	US-09-865-198-4
3	48	100.0	105	9	US-09-982-107-12
4	48	100.0	106	10	US-09-976-787-24
5	48	100.0	106	10	US-09-865-198-23
6	48	100.0	107	9	US-09-144-886-76
7	48	100.0	107	9	US-09-144-886-82
8	48	100.0	107	9	US-09-144-886-83
9	48	100.0	107	9	US-09-144-886-88
10	48	100.0	108	10	US-09-976-787-8
11	48	100.0	108	10	US-09-865-198-8
12	48	100.0	238	10	US-09-976-787-29
13	48	100.0	238	10	US-09-865-198-28
14	48	100.0	240	10	US-09-976-787-28
15	48	100.0	240	10	US-09-865-198-27
16	47	97.9	119	10	US-09-808-037-28
17	47	97.9	239	10	US-09-808-037-6
18	45	93.8	10	10	US-09-910-059-26
19	45	93.8	107	10	US-09-910-059-50

20	45	93.8	107	10	US-09-910-059-61	Sequence 61, Appl
21	45	93.8	107	10	US-09-910-059-65	Sequence 65, Appl
22	45	93.8	107	10	US-09-910-059-71	Sequence 71, Appl
23	45	93.8	108	10	US-09-910-059-9	Sequence 9, Appl
24	45	93.8	235	10	US-09-910-059-17	Sequence 17, Appl
25	45	93.8	235	10	US-09-910-059-52	Sequence 52, Appl
26	45	93.8	235	10	US-09-910-059-97	Sequence 97, Appl
27	45	93.8	235	10	US-09-910-059-99	Sequence 99, Appl
28	44	91.7	10	9	US-09-771-415-3	Sequence 3, Appl
29	44	91.7	10	9	US-09-996-288-14	Sequence 14, Appl
30	44	91.7	10	10	US-09-796-848A-5	Sequence 5, Appl
31	44	91.7	106	9	US-09-771-415-1	Sequence 1, Appl
32	44	91.7	106	9	US-09-771-415-17	Sequence 17, Appl
33	44	91.7	106	9	US-09-771-415-19	Sequence 19, Appl
34	44	91.7	106	9	US-09-771-415-21	Sequence 21, Appl
35	44	91.7	106	9	US-09-771-415-23	Sequence 23, Appl
36	44	91.7	106	9	US-09-771-415-25	Sequence 25, Appl
37	44	91.7	106	9	US-09-996-288-13	Sequence 13, Appl
38	44	91.7	106	9	US-09-996-288-54	Sequence 54, Appl
39	44	91.7	106	9	US-09-996-288-56	Sequence 56, Appl
40	44	91.7	106	9	US-09-996-288-57	Sequence 57, Appl
41	44	91.7	106	9	US-09-996-288-59	Sequence 59, Appl
42	44	91.7	106	9	US-09-996-288-60	Sequence 60, Appl
43	44	91.7	106	9	US-09-996-288-62	Sequence 62, Appl
44	44	91.7	106	9	US-09-996-288-64	Sequence 64, Appl
45	44	91.7	106	9	US-09-996-288-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-976-787-4

; Sequence 4, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-4

Query Match 100.0%; Score 48; DB 10; Length 10;
Best Local Similarity 100.0%; Pred No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 1 SASSSVSVMH 10

RESULT 2

US-09-865-198-4

; Sequence 4, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-4

Query Match 100.0%; Score 48; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
Db 1 SASSSVSVMH 10

RESULT 3
US-09-982-107-12
; Sequence 12; Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIAVAT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982.107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12

Query Match 100.0%; Score 48; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
Db 24 SASSSVSVMH 33

RESULT 4
US-09-976-787-24
; Sequence 24; Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46305
; CURRENT APPLICATION NUMBER: US/09/976.787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
Db 24 SASSSVSVMH 33

RESULT 5
US-09-865-198-23
; Sequence 23; Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
Db 24 SASSSVSVMH 33

RESULT 6
US-09-144-886-76
; Sequence 76; Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C9 region VL epitope 1
US-09-144-886-76

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
Db 24 SASSSVSVMH 33

RESULT 7

US-09-144-886-82
; Sequence 82, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1E8 region VL epitope 1
US-09-144-886-82

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
|||||
DB 24 SASSSVSYMH 33

RESULT 8
US-09-144-886-83
; Sequence 83, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1G7 region VL epitope 1
US-09-144-886-83

Query Match 100.0%; Score 48; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
|||||
DB 24 SASSSVSYMH 33

RESULT 9
US-09-144-886-88
; Sequence 88, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO

; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/a clone
; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88

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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
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DB 24 SASSSVSYMH 33

RESULT 10
US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
|||||
DB 24 SASSSVSYMH 33

RESULT 11
US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse

US-09-865-198-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
|||||

Db 24 SASSSVSVMH 33

RESULT 12

US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US 09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
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Db 156 SASSSVSVMH 165

RESULT 13

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
|||||

Db 156 SASSSVSVMH 165

RESULT 14

US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
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Db 156 SASSSVSVMH 165

RESULT 15

US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
|||||

Db 156 SASSSVSVMH 165

Search completed: December 23, 2002, 07:58:18
Job time : 0.930233 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 1.97674 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-4

Perfect score: 48

Sequence: 1 SASSSVSYMH 10

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Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	48	100.0	91	2	SI7637
3	48	100.0	91	2	SI7639
4	48	100.0	94	2	S20650
5	48	100.0	94	2	S20653
6	48	100.0	97	2	S26341
7	48	100.0	97	2	PH1084
8	48	100.0	99	2	D38601
9	48	100.0	100	2	S29590
10	48	100.0	102	2	SI1115
11	48	100.0	102	2	S24214
12	48	100.0	103	2	S29591
13	48	100.0	104	2	B49049
14	48	100.0	106	2	B54378
15	48	100.0	106	2	PS0071
16	48	100.0	106	2	PS0072
17	48	100.0	106	2	SI1114
18	48	100.0	106	2	SI1120
19	48	100.0	107	1	KVMSX4
20	48	100.0	107	2	A30562
21	48	100.0	107	2	B30562
22	48	100.0	107	2	PT0395
23	48	100.0	107	2	PT0398
24	48	100.0	107	2	PT0399
25	48	100.0	107	2	PT0400
26	48	100.0	107	2	PT0401
27	48	100.0	107	2	PT0402
28	48	100.0	107	2	PT0403
29	48	100.0	107	2	SI1112

```

30 48 100.0 107 2 SI1113 Ig kappa chain V r
31 48 100.0 107 2 SI1116 Ig kappa chain V r
32 48 100.0 107 2 SI1117 Ig kappa chain V r
33 48 100.0 107 2 SI1118 Ig kappa chain V r
34 48 100.0 107 2 SI1119 Ig kappa chain V r
35 48 100.0 107 2 SI1121 Ig kappa chain V r
36 48 100.0 107 2 SI1123 Ig kappa chain V r
37 48 100.0 107 2 PT0406 Ig kappa chain V r
38 48 100.0 108 2 G30560 Ig kappa chain V r
39 48 100.0 130 1 PL0079 Ig kappa chain pre
40 48 100.0 140 2 PL0013 Ig kappa chain pre
41 47 97.9 107 2 PD0011 Ig kappa chain V r
42 47 97.9 107 2 PC4405 Ig kappa chain V r
43 45 93.8 76 2 A48784 Ig kappa V regions
44 45 93.8 91 2 SI7626 Ig kappa chain V r
45 44 91.7 91 2 SI7628 Ig kappa chain V r

```

ALIGNMENTS

RESULT 1

SI7629

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: SI7629

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: SI7230; MUID:91326098; PMID:1907718

A:Accession: SI7629

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-91 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 0.0079;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

|||||

Db 16 SASSSVSYMH 25

RESULT 2

SI7637

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: SI7637

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: SI7230; MUID:91326098; PMID:1907718

A:Accession: SI7637

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-91 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 0.0079;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

|||||

Db 16 SASSSVSYMH 25


```

RESULT 8
D38601
Ig kappa chain V region (6A7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: D38601
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: D38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <GOS>
A:Cross-references: GB:M57981; NID:q196408; PIDN:AAA63362.1; PID:g196409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
   |||||
Db 16 SASSSVSVMH 25

RESULT 9
S29590
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S29590
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S29590
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <KAV>
A:Cross-references: EMBL:X59093; NID:g52225; PIDN:CAA41819.1; PID:g52226
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
   |||||
Db 24 SASSSVSVMH 33

RESULT 10
S1115
Ig kappa chain V region (clone NQ2-20.5.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S1115
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazalone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S1115
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <KAA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-84/Domain: immunoglobulin homology <IMM>
```

```

Query Match      100.0%; Score 48; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
   |||||
Db 24 SASSSVSVMH 33

RESULT 11
S24214
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24214
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular ex
A:Reference number: S24214; MUID:91217618; PMID:1902500
A:Accession: S24214
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <SHI>
A:Cross-references: EMBL:X58204
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-87/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
   |||||
Db 22 SASSSVSVMH 31

RESULT 12
S29591
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S29591
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S29591
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <KAV>
A:Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 48; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
   |||||
Db 23 SASSSVSVMH 32

RESULT 13
B49049
Ig kappa chain V region (anti-idiotypic) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49049
R:Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A:Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR ant
```

A:Reference number: A49049; MUID:93049629; PMID:1425914
A:Accession: B49049
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-104 <ARM>
A:Experimental source: BALB/c
A>Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIP:118299)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
DB 24 SASSSVSVMH 33

RESULT 14

B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B54378
R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
A:Reference number: A54378; MUID:94165109; PMID:7509814
A:Accession: B54378
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <AGA>
A:Cross-references: GB:S68985; NID:g545746; PID:RAB30096.1; PID:g545747
A:Experimental source: spleen and myeloma cell line MOPC 315.43
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
DB 24 SASSSVSVMH 33

RESULT 15

PS0071
Ig kappa chain V region (38C13.V8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0071
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0071
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
DB 24 SASSSVSVMH 33

Search completed: December 23, 2002, 07:31:35
Job time : 1.97674 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 0.988372 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSVMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	48	100.0	107	1 KV6A_MOUSE	P01675 mus musculus
2	48	100.0	107	1 KV6B_MOUSE	P01676 mus musculus
3	48	100.0	107	1 KV6C_MOUSE	P01677 mus musculus
4	48	100.0	107	1 KV6D_MOUSE	P01678 mus musculus
5	48	100.0	107	1 KV6E_MOUSE	P04940 mus musculus
6	48	100.0	107	1 KV6F_MOUSE	P04941 mus musculus
7	48	100.0	107	1 KV6H_MOUSE	P04942 mus musculus
8	48	100.0	107	1 KV6I_MOUSE	P04943 mus musculus
9	48	100.0	107	1 KV6J_MOUSE	P04944 mus musculus
10	42	87.5	108	1 KV6K_MOUSE	P04945 mus musculus
11	36	75.0	107	1 KV6E_MOUSE	P01679 mus musculus
12	34	70.8	129	1 KV4A_MOUSE	P01680 mus musculus
13	34	70.8	270	1 ALYS_BPRIT	Q38135 bacterioph
14	34	70.8	731	1 BGAL_MALDO	P48981 malus domes
15	33	68.8	271	1 RRF_SPIOL	P82231 spinacia ol
16	33	68.8	405	1 CBG_HUMAN	P08185 homo sapien
17	32	66.7	394	1 DUS4_HUMAN	Q13115 homo sapien
18	32	66.7	933	1 SIAP_CAMEF	P35827 campylobact
19	31	64.6	230	1 YIME_BACSU	O31727 bacillus su
20	31	64.6	318	1 ATH4_ARATH	P92953 arabidopsis
21	31	64.6	377	1 Y835_METJA	Q58245 methanococc
22	31	64.6	460	1 MYIN_HELPJ	Q92kw7 helicobacte
23	31	64.6	461	1 MYIN_HELPJ	O25551 helicobacte
24	31	64.6	989	1 PTP3_DICDI	P54637 dictyosteli
25	31	64.6	1380	1 ZMS1_YEAST	P46974 saccharomyc
26	31	64.6	1520	1 PMPD_CHLMU	Q9plb0 chlamydia m
27	30	62.5	218	1 NUKM_ARATH	Q42577 arabidopsis
28	30	62.5	367	1 CCR3_MOUSE	O88410 mus musculus
29	30	62.5	368	1 CCR3_HUMAN	P49682 homo sapien
30	30	62.5	383	1 CBG_RABIT	P33775 oryctolagus
31	30	62.5	418	1 HLT_VIBFA	Q99289 vibrio para
32	30	62.5	435	1 FUT9_ARATH	Q9xi77 arabidopsis
33	30	62.5	447	1 COBB_METTH	O27509 methanobact

RESULT 1

ID	KV6A_MOUSE	STANDARD	PRT	107 AA
AC	P01675;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-VI region XRPC 44.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79082830; PubMed=103573;			
RA	Rao D.N., Rudikoff S., Potter M.;			
RT	"k Chain variable regions from three galactan binding myeloma			
RT	proteins.";			
RL	Biochemistry 17:5555-5559(1978).			
CC	-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT			
CC	BIND GALACTAN.			
DR	PIR: A01941; KVMX4.			
DR	HSSP; P01679; 2FBJ.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
KW	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 33			
FT	DOMAIN 34 48			
FT	DOMAIN 49 55			
FT	DOMAIN 56 87			
FT	DOMAIN 88 96			
FT	DOMAIN 97 106			
FT	DISULFID 23 87			
FT	NON_TER 107 107			
SQ	SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;			

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
| | | | | | | | | |
Db 24 SASSSVSVMH 33

RESULT 2

ID	KV6B_MOUSE	STANDARD	PRT	107 AA
AC	P01676;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-VI region XRPC 24.			

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins";
RL Biochemistry 17:5555-5559(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR PIR: A01941; KVMX4.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11584 MW; 366D022A5EC34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
DB 24 SASSSVSVMH 33
IIIIIIIIII

RESULT 3
KV6C_MOUSE STANDARD; PRT; 107 AA.
ID KV6C_MOUSE
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 601).
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins";
RL Biochemistry 17:5555-5559(1978).
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
THAT BIND GALACTAN.
DR PIR: A01941; KVMX4.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
DB 24 SASSSVSVMH 33
IIIIIIIIII

RESULT 4
KV6D_MOUSE STANDARD; PRT; 107 AA.
ID KV6D_MOUSE
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region SAPC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "kappa Chain joining segments and structural diversity of antibody
combining sites";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR PIR: A01941; KVMX4.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
DB 24 SASSSVSVMH 33
IIIIIIIIII

RESULT 5
KV6F_MOUSE


```

ID  KV6_MOUSE  STANDARD;          PRT;   107 AA.
AC  P04940;
DT  13-AUG-1987 (Rel. 05, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-VI region NQ2-17.4.1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83271467; PubMed=6877353;
RA  Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT  "mRNA sequences define an unusually restricted IgG response to 2-
RT  phenylloxazalone and its early diversification.";
RL  Nature 304:320-324(1983).
CC  -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; K00735; AAA38680.1; -.
DR  HSP; P01679; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
KW  Immunoglobulin V region; Hybridoma.
FT  DOMAIN 1 23
FT  DOMAIN 24 33
FT  DOMAIN 34 48
FT  DOMAIN 49 55
FT  DOMAIN 56 87
FT  DOMAIN 88 96
FT  DOMAIN 97 106
FT  DISULFID 23 87
FT  NON_TER 107 107
SQ  SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68E6 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SASSSVSYMH 10
DB  24 SASSSVSYMH 33

RESULT 6
KV6G_MOUSE  STANDARD;          PRT;   107 AA.
ID  KV6G_MOUSE  STANDARD;          PRT;   107 AA.
AC  P04941;
DT  13-AUG-1987 (Rel. 05, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-VI region NQ2-48.2.2.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83271467; PubMed=6877353;
RA  Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT  "mRNA sequences define an unusually restricted IgG response to 2-
RT  phenylloxazalone and its early diversification.";
RL  Nature 304:320-324(1983).

```

```

CC  -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC  -----
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CC  -----
DR  EMBL; K00737; AAA38682.1; -.
DR  HSP; P01679; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
KW  Immunoglobulin V region; Hybridoma.
FT  DOMAIN 1 23
FT  DOMAIN 24 33
FT  DOMAIN 34 48
FT  DOMAIN 49 55
FT  DOMAIN 56 87
FT  DOMAIN 88 96
FT  DOMAIN 97 106
FT  DISULFID 23 87
FT  NON_TER 107 107
SQ  SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SASSSVSYMH 10
DB  24 SASSSVSYMH 33

RESULT 7
KV6H_MOUSE  STANDARD;          PRT;   107 AA.
ID  KV6H_MOUSE  STANDARD;          PRT;   107 AA.
AC  P04942;
DT  13-AUG-1987 (Rel. 05, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-VI region NQ5-61.1.2.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83271467; PubMed=6877353;
RA  Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT  "mRNA sequences define an unusually restricted IgG response to 2-
RT  phenylloxazalone and its early diversification.";
RL  Nature 304:320-324(1983).
CC  -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC  -----
DR  EMBL; K00739; AAA38684.1; -.
DR  HSP; P01679; 2FBJ.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
KW  Immunoglobulin V region; Hybridoma.

```

FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11605 MW; CAGC4284ECFCB550 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 24 SASSSVSYMH 33

RESULT 8

ID KV6L_MOUSE STANDARD; PRT; 107 AA.
AC P04943;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-VI region NQ6-8.3.1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-

phenyloxazolone and its early diversification.";

RL Nature 304:320-324(1983).

CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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EMBL; K00740; AAA38685.1; -

HSSP; P01679; 2FBJ.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Hybridoma.

DOMAIN 1 23

DOMAIN 24 33

DOMAIN 34 48

DOMAIN 49 55

DOMAIN 56 87

DOMAIN 88 96

DOMAIN 97 106

DISULFID 23 87

NON_TER 107 107

SEQUENCE 107 AA; 11572 MW; 6F694824ECFCB65 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0034;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

RESULT 9

ID KV6J_MOUSE

AC P04944;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-VI region NQ5-78.2.6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-

phenyloxazolone and its early diversification.";

RL Nature 304:320-324(1983).

CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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EMBL; K00744; AAA38689.1; -

HSSP; P01679; 2FBJ.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Hybridoma.

DOMAIN 1 23

DOMAIN 24 33

DOMAIN 34 48

DOMAIN 49 55

DOMAIN 56 87

DOMAIN 88 96

DOMAIN 97 106

DISULFID 23 87

NON_TER 107 107

SEQUENCE 107 AA; A38290781F3C30D3 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0034;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

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Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

Db 24 SASSSVSYMH 33

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RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K00746; AAA38691.1; -.
CC HSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 98
FT DOMAIN 99 108
FT DISULFID 23 87
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
Query Match 87.5%; Score 42; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASSSVSVMH 10
Db 24 SASSSVSVMY 33
|||||||:|
RESULT 11
KV6E_MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RP MEDLINE=88217852; PubMed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01942; KVM5J5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR003006; Ig_MHC.

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```

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT STRAND 4 7
FT STRAND 10 14
FT TURN 15 16
FT TURN 19 25
FT STRAND 31 37
FT STRAND 39 40
FT TURN 44 48
FT STRAND 52 53
FT STRAND 55 56
FT TURN 59 60
FT TURN 61 66
FT TURN 67 68
FT STRAND 69 74
FT HELIX 79 81
FT STRAND 83 91
FT TURN 92 93
FT STRAND 94 97
FT STRAND 101 106
FT NON_TER 107 107
FT SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;
Query Match 75.0%; Score 36; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SASSSVSVMH 10
Db 24 SASSSVSVMY 33
|||||||:|
RESULT 12
KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -!- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
CC -----
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Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
 |||: ||||

Db 40 SATNEASVMH 49

RESULT 14

BGAL_MALDO
 ID BGAL_MALDO STANDARD; PRT; 731 AA.

AC P48981;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-galactosidase) (Exo-(1->4)-beta-D-galactanase).

DE galactosidase)

DE Malus domestica (Apple) (Malus sylvestris).

OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC Eucotyledons I; Rosales; Rosaceae; Maloideae; Malus.

NCBI_TaxID=3750;

FN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=cv. Granny Smith; TISSUE=Fruit cortical tissue;

RX MEDLINE=95083752; PubMed=7991682;

RT Ross G.S., Wegryn T., Macrae E.A., Redgwell R.J.;

RT "Apple beta-galactosidase. Activity against cell wall polysaccharides and characterization of a related cDNA clone.";

RL Plant Physiol. 106:521-528(1994).

CC -1- FUNCTION: Involved in cell wall degradation. Degrades polysaccharides containing beta-(1->4)-linked galactans, acting as an exo-(1->4)-beta-D-galactanase.

CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.

CC -1- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.

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EMBL: L29451; AAA62324.1; -.

InterPro: IPR001944; GH_35.

DR Pfam: PF01301; Glyco_hydro_35; 1.

DR PRINTS; PR00742; GLHYDRLASE35.

DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.

KW Hydrolase; Glycosidase; Signal.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 731 BETA-GALACTOSIDASE.

FT ACT_SITE 182 182 PROTON DONOR (POTENTIAL).

FT ACT_SITE 251 251 NUCLEOPHILE (POTENTIAL).

SQ SEQUENCE 731 AA; 80995 MW; FAB65D24A0D30BD4 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 731;

Best Local Similarity 70.0%; Pred. No. 22;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
 :||:||||

Db 21 AASASVSYDH 30

RESULT 15

RRE_SPIOL
 ID RRE_SPIOL STANDARD; PRT; 271 AA.

AC P82231; Q9XG97;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ribosome recycling factor, chloroplast precursor (Ribosome

```

DE releasing factor, chloroplast) (RRF) (CpFrr) (RRFHCP).
GN RRF OR FRHCP.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 79-88.
RC TISSUE=Leaf;
RX MEDLINE=99254063; PubMed=10318906;
RA Rolland N., Janosi L., Block M.A., Shuda M., Teyssier E., Miede C.,
RA Cheniclet C., Carde J.-P., Kaji A., Joyard J.;
RT "Plant ribosome recycling factor homologue is a chloroplastic protein
RT and is bactericidal in Escherichia coli carrying temperature-sensitive
RT ribosome recycling factor";
RL Proc. Natl. Acad. Sci. U.S.A. 96:5464-5469(1999).
RN [2]
RN SEQUENCE OF 79-99 AND 194-217.
RC STRAIN=cv. Alvaro; TISSUE=Leaf;
RX PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: RESPONSIBLE FOR THE RELEASE OF RIBOSOMES FROM MESSENGER
CC RNA AT THE TERMINATION OF CHLOROPLASTIC PROTEIN BIOSYNTHESIS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST. THE MAJOR PART WAS FOUND IN THE
CC STROMA AND SOME PROTEIN WAS IN THE ENVELOPE SUBFRACTION, BUT NO
CC PROTEIN WAS DETECTED IN THE THYLAKOIDS.
CC -!- TISSUE SPECIFICITY: RESTRICTED TO PHOTOSYNTHETIC TISSUES.
CC -!- MISCELLANEOUS: EXPRESSION SEEMS TO BE LIGHT-INDEPENDANT.
CC -!- SIMILARITY: BELONGS TO THE RRF FAMILY.
CC -----
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CC -----
DR EMBL: AJ133751; CAB41419.1; -
DR HSP: O9X1B9; 1DD5
DR InterPro: IPR002861; RRF.
DR Pfam: PF01765; RRF; 1.
DR TIGRFAMs: TIGR00496; frr; 1.
KW Protein biosynthesis; Transit peptide; Chloroplast.
FT TRANSIT 1 78
FT CHAIN 79 271 RIBOSOME RECYCLING FACTOR.
SQ SEQUENCE 271 AA; 30431 MW; F7D3012BB90ADI75 CRC64;

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Query Match          68.8%; Score 33; DB 1; Length 271;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 SASSSVSYMH 10
   | | | | |
DB 5 SLSSATSYLH 14

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Search completed: December 23, 2002, 07:26:06
Job time : 1.98837 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 4.14729 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	97.9	134	11 Q8VDD0	Q8VDD0 mus musculu
2	44	91.7	97	11 Q9JL76	Q9JL76 mus musculu
3	43	89.6	235	11 Q91W12	Q91W12 mus musculu
4	38	79.2	106	5 Q9U410	Q9U410 schistosoma
5	37	77.1	547	2 Q59117	Q59117 arthrobacte
6	37	77.1	858	5 Q9V429	Q9V429 drosophila
7	36	75.0	991	5 Q9VIF5	Q9VIF5 drosophila
8	35	72.9	200	3 Q08003	Q08003 saccharomyc
9	35	72.9	689	5 Q8T6L8	Q8T6L8 drosophila
10	35	72.9	720	3 Q14367	Q14367 schizosacch
11	35	72.9	1004	16 Q84646	Q84646 chlamydia t
12	35	72.9	1313	5 Q8T6L9	Q8T6L9 drosophila
13	34	70.8	537	16 Q98L15	Q98L15 rhizobium l
14	34	70.8	731	10 Q9AY51	Q9AY51 pyrus pyrif
15	34	70.8	1095	10 Q9C7S5	Q9C7S5 arabidopsis
16	34	70.8	1430	5 Q9W0B0	Q9W0B0 drosophila

17	34	70.8	1501	10 Q94LS3	Q94LS3 oryza sativ
18	34	70.8	2136	10 Q9SL97	Q9SL97 arabidopsis
19	33	68.8	101	11 Q9JL78	Q9JL78 mus musculu
20	33	68.8	234	3 Q94664	Q94664 schizosacch
21	33	68.8	347	8 Q9MM74	Q9MM74 acanthodact
22	33	68.8	382	2 Q9AMN1	Q9AMN1 clostridium
23	33	68.8	463	11 Q991C4	Q991C4 mus musculu
24	33	68.8	477	16 Q97TF8	Q97TF8 clostridium
25	33	68.8	669	10 Q9SLC7	Q9SLC7 arabidopsis
26	33	68.8	677	5 Q17720	Q17720 caenorhabdi
27	33	68.8	841	5 Q9VC32	Q9VC32 drosophila
28	33	68.8	944	5 Q18137	Q18137 caenorhabdi
29	33	68.8	1148	5 Q95ZV7	Q95ZV7 caenorhabdi
30	33	68.8	1480	5 Q18138	Q18138 caenorhabdi
31	32	66.7	95	10 Q9M3C7	Q9M3C7 arabidopsis
32	32	66.7	158	10 Q9SIH6	Q9SIH6 arabidopsis
33	32	66.7	206	5 Q9VK13	Q9VK13 drosophila
34	32	66.7	219	16 Q9KBL2	Q9KBL2 bacillus ha
35	32	66.7	240	16 Q9KRV9	Q9KRV9 vibrio chol
36	32	66.7	264	5 Q97455	Q97455 caenorhabdi
37	32	66.7	273	10 Q9SA31	Q9SA31 arabidopsis
38	32	66.7	288	5 Q19536	Q19536 caenorhabdi
39	32	66.7	294	1 Q74060	Q74060 cenarchaeum
40	32	66.7	303	4 Q9NSW1	Q9NSW1 homo sapien
41	32	66.7	363	16 Q9K9P1	Q9K9P1 bacillus ha
42	32	66.7	393	3 Q8X0D9	Q8X0D9 neurospora
43	32	66.7	411	4 Q13649	Q13649 homo sapien
44	32	66.7	451	16 Q9RK08	Q9RK08 streptomyce
45	32	66.7	510	16 Q9K3J1	Q9K3J1 streptomyce

ALIGNMENTS

RESULT 1

Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Sembi P.;
RT "Targeting T cells to the CNS";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; I.
DR SMART; SM00409; IG; I.
DR SMART; SM00406; IGV; I.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 97.9%; Score 47; DB 11; Length 134;
Best Local Similarity 90.0%; Pred. No. 0.026;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 46 SASSSVSYMH 55

RESULT 2

Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RA MEDLINE=20448942; PubMed=10992488;
RX Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -;
DR HSSP; P03679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;

Query Match 91.7%; Score 44; DB 11; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASSSVSYMH 10
Db 15 ASSSVSYMH 23

RESULT 3

Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEED5E8FEF CRC64;

Query Match 89.6%; Score 43; DB 11; Length 235;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10

Db 46 SASSSVSYMH 55

RESULT 4

Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -;
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 79.2%; Score 38; DB 5; Length 106;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
Db 24 SASSSVSYMH 33

RESULT 5

Q59117 PRELIMINARY; PRT; 547 AA.
AC Q59117;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Choline oxidase (EC 1.1.3.17).
GN CODA.
OS Arthrobacter globiformis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=1665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96145502; PubMed=8555454;
RA Deshnlum P., Los D.A., Hayashi H., Mustardy L., Murata N.;
RT "Transformation of *Synechococcus* with a gene for choline oxidase
RT enhances tolerance to salt stress.";
RL Plant Mol. Biol. 29:897-907(1995).
DR EMBL; X84895; CAA59321.1; -;
DR HSSP; P22637; 3COX.
DR InterPro; IPR000172; GMC_oxred.
DR Pfam; PF00732; GMC_oxred; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
KW Oxidoreductase.
SQ SEQUENCE 547 AA; 58865 MW; 589175892034B3BE CRC64;

Query Match 77.1%; Score 37; DB 2; Length 547;
Best Local Similarity 77.8%; Pred. No. 16;


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Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASSSVSYMH 10
Db 208 SSSVSYSIH 216

RESULT 6
Q9V429 PRELIMINARY; PRT; 858 AA.
AC Q9V429;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CG11770 protein (LINES).
GN LIN OR CG11770.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA W.K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AF22358; AAF59024.1; -.
DR FlyBase; FBgn0032920; CG9252.
SQ SEQUENCE 991 AA; 111757 MW; FFD72B5E86384155 CRC64;

SEQUENCE FROM N.A.
RX MEDLINE=20296724; PubMed=10837029;
RA Hatini V., Bokor P., Goto-Mandeville R., DiNardo S.;
RT "Tissue- and stage-specific modulation of wingless signaling by the
segment polarity gene lines."
RL Genes Dev. 14:1364-1376(2000).
DR EMBL; AE003835; AAF59024.1; -.
DR EMBL; AF272358; AAF76228.1; -.
DR FlyBase; FBgn0002552; lin.
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SQ SEQUENCE 858 AA; 96291 MW; 95030ED5FE096139 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 858;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 366 STEASVSIMH 375

RESULT 7
Q9VIF5 PRELIMINARY; PRT; 991 AA.
AC Q9VIF5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE CG9252 protein.
GN CG9252.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003669; AAF53964.1; -.
DR FlyBase; FBgn0032920; CG9252.
SQ SEQUENCE 991 AA; 111757 MW; FFD72B5E86384155 CRC64;

Query Match 75.0%; Score 36; DB 5; Length 991;
Best Local Similarity 70.0%; Pred. No. 50;
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Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
:|||||
Db 927 NASKSVSYMH 936

RESULT 8

ID Q08003 PRELIMINARY; PRT; 200 AA.
AC Q08003;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chromosome XII reading frame ORF YLR073C.
GN YLR073C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Pohl T.M.
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 273245; CAA97630.1; -.
DR SGD; S0004063; YLR073C.
SQ SEQUENCE 200 AA; 22850 MW; 1C93378ED78C41A4 CRC64;

Query Match: 72.9%; Score 35; DB 3; Length 200;

Best Local Similarity 70.0%; Pred. No. 15;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10

Db 75 SSSSSSYIH 84
:|||||

RESULT 9

ID Q8T6L8 PRELIMINARY; PRT; 689 AA.
AC Q8T6L8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Unconventional myosin 29D short isoform.
GN MYO29D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R.; TISSUE=OVARY;
RA Tzolovskiy G., Bowes M., Millo H., Pathirana S., Wood T.;
RT "Identification and phylogenetic analysis of Drosophila melanogaster myosins";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AF454349; AAL91723.1; -.
SQ SEQUENCE 689 AA; 74009 MW; 9525A3C5B928FD2A CRC64;

Query Match: 72.9%; Score 35; DB 5; Length 689;

Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10

Db 613 ASSSVSFLH 622
:|||||

RESULT 10

ID O14367 PRELIMINARY; PRT; 720 AA.
AC O14367;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE GLUCONATE.
GN GTII.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP.011;
RX MEDLINE=98039718; PubMed=9372449;
RA Caspari T.;
RT "Onset of gluconate-H⁺ symport in Schizosaccharomyces pombe is regulated by the kinases Wis1 and Pka1, and requires the gti1+ gene product.";
RL J. Cell Sci. 110:2599-2608(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP.011;
RX STRAIN=SP.011;
RA Caspari T.;
RT product.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Zimmermann W., Wambutt R., McDougall R.C., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; X92655; CAA63345.1; -.
DR EMBL; AL133154; CAB61447.1; -.
SQ SEQUENCE 720 AA; 78725 MW; 5CC2CD58ACE7CD87 CRC64;

Query Match: 72.9%; Score 35; DB 3; Length 720;

Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASSSVSYMH 10

Db 255 SSSSLSYLH 263
:|||||

RESULT 11

ID O84646 PRELIMINARY; PRT; 1004 AA.
AC O84646;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Exodeoxyribonuclease V, gamma.
GN RECC OR CT640.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis";
RL Science 282:754-759(1998).
DR EMBL; AE001334; AAC68244.1; -.
KW Complete proteome.
SQ SEQUENCE 1004 AA; 114401 MW; BB89266ED55F1496 CRC64;

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SQ SEQUENCE 537 AA; 58507 MW; 250E2948450EC19D CRC64;
  Query Match 72.9%; Score 35; DB 16; Length 1004;
  Best Local Similarity 70.0%; Pred. No. 83;
  Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
   :||| ||| |
Db 108 SSSEVSYSYH 117

RESULT 12
Q876L9 PRELIMINARY; PRT; 1313 AA.
AC Q876L9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Unconventional myosin 29D.
GN MYO29D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R; TISSUE=OVARY;
RA Tzolovsky G., Bowles M., Millo H., Pathirana S., Wood T.;
RT "Identification and phylogenetic analysis of Drosophila melanogaster
  myosins.";
RL Mol. Biol. Evol. 0:0-0(2002).
DR EMBL; AF454348; AAL91722.1; -.
SQ SEQUENCE 1313 AA; 142708 MW; 1A164E5A073D9450 CRC64;

  Query Match 72.9%; Score 35; DB 5; Length 1313;
  Best Local Similarity 60.0%; Pred. No. 1.le+02;
  Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
   :||| ||| |
Db 1237 AASSVSLH 1245

RESULT 13
Q98LI5 PRELIMINARY; PRT; 537 AA.
AC Q98LI5;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable dehydrogenase.
GN MLL1008.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Ishikawa A., Kawashima K., Kimura T.,
RA Watanabe A., Idesawa K., Ishikawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
  Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002996; BAB48478.1; -.
DR InterPro; IPR000172; GMC_oxred.
DR Pfam; PF00732; GMC_oxred; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
KW Complete proteome.

SQ SEQUENCE 537 AA; 58507 MW; 250E2948450EC19D CRC64;
  Query Match 70.8%; Score 34; DB 10; Length 731;
  Best Local Similarity 70.0%; Pred. No. 97;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
   :||| ||| |
Db 21 AASASVSVDH 30

RESULT 15
Q9C7S5 PRELIMINARY; PRT; 1095 AA.
AC Q9C7S5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Leucine-rich receptor-like protein kinase, putative, 84911-81624
  (Putative leucine-rich receptor protein kinase).
GN T9N14.20 OR ATLG72300.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
```

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.D., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Militichev J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yui G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequences and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana"; 816-820(2000).
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC067754; AAGS1803.1; -;
DR EMBL; AY080797; AAL87278.1; -;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR002290; Ser_chr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 15.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00369; LRR_TIP; 6.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 1095 AA; 121520 MW; 52DECA8C2E0669BA CRC64;
Query Match 70.8%; Score 34; DB 10; Length 1095;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ASSSVSYNH 10
Db 910 ASSGLAYMH 918

Search completed: December 23, 2002, 07:29:50
Job time : 7.14729 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 : Search time 0.69186 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	90.3	204	1 YIP8_YEAST	P40451 saccharomyc
2	28	90.3	531	1 VLI1_HPV16	P03101 human papil
3	28	90.3	601	1 YFK5_SCHPO	P87132 schizosacch
4	28	90.3	707	1 YJ9C_YEAST	P47166 saccharomyc
5	27	87.1	108	1 KV6K_MOUSE	P04945 mus musculu
6	27	87.1	126	1 YRP2_IRV6	P18306 chilo iride
7	27	87.1	129	1 KV4A_MOUSE	P01680 mus musculu
8	27	87.1	219	1 TR23_YEAST	Q03784 saccharomyc
9	27	87.1	255	1 YFCA_HAEIN	P46490 haemophilus
10	27	87.1	720	1 GTSE_HUMAN	Q9nyz3 homo sapien
11	27	87.1	919	1 YB03_YEAST	P38073 saccharomyc
12	27	87.1	1477	1 KELC_DROME	Q04652 drosophila
13	26	83.9	87	1 IM08_YEAST	P57744 saccharomyc
14	26	83.9	173	1 SP12_YEAST	P17123 saccharomyc
15	26	83.9	334	1 EI3B_HORVU	P15737 hordeum vul
16	26	83.9	348	1 YK51_YEAST	P36152 saccharomyc
17	26	83.9	352	1 NPTI_ASPOR	P46076 aspergillus
18	26	83.9	382	1 YAE8_SCHPO	Q03848 schizosacch
19	26	83.9	469	1 VIZ2_BPV1	P03109 bovine papil
20	26	83.9	614	1 TUI1_SCHPO	Q03715 schizosacch
21	26	83.9	687	1 YBGO_YEAST	P34225 saccharomyc
22	26	83.9	1050	1 ULK1_HUMAN	O75385 homo sapien
23	26	83.9	1398	1 MHP1_YEAST	P43638 saccharomyc
24	26	83.9	2504	1 FAS_HUMAN	P49327 homo sapien
25	26	83.9	2895	1 HYD_DROME	P51592 drosophila
26	25	80.6	209	1 V281_ARATH	Q959t7 arabidopsis
27	25	80.6	310	1 YG63_SYNY3	P74068 synecocyst
28	25	80.6	371	1 RLPA_ANASP	O8y5z4 anabaena sp
29	25	80.6	444	1 NUAM_LOCHI	Q36424 locusta mig
30	25	80.6	604	1 SP20_YEAST	P50875 saccharomyc
31	25	80.6	735	1 TFPA_YEAST	P41895 saccharomyc
32	25	80.6	838	1 FAS_MOUSE	P19096 mus musculu
33	25	80.6	932	1 HIRL_SCHPO	P87314 schizosacch

34 25 80.6 1060 1 YN18_YEAST P53836 saccharomyc
35 25 80.6 1090 1 CYA2_RAT P26769 rattus norv
36 25 80.6 1177 1 JAK2_DROME Q24592 drosophila
37 25 80.6 1275 1 YAU9_SCHPO Q10164 schizosacch
38 25 80.6 1356 1 ROM2_YEAST P51862 saccharomyc
39 25 80.6 1489 1 YGPO_YEAST P53115 saccharomyc
40 25 80.6 1569 1 GLI3_XENLA Q91660 xenopus lae
41 25 80.6 2505 1 FAS_RAT P12785 rattus norv
42 24 77.4 103 1 YAA0_MYCPN P75074 mycoplasma
43 24 77.4 145 1 Y657_ARCFU O29600 archaeoglob
44 24 77.4 154 1 YF12_MYCPN P73274 mycoplasma
45 24 77.4 167 1 Y420_RICPR Q9zdb2 rickettsia

ALIGNMENTS

RESULT 1

YIP8_YEAST
ID YIP8_YEAST STANDARD; PRT; 204 AA.
AC P40451.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 22.8 kDa protein in FOX3-UBP7 intergenic region.
GN YII158W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churche C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajadream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YKR100C.
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CC -----
CC EMBL: Z38059; CAA86120.1; -
CC PIR: S48376; S48376
CC SGD: S0001420; YII158W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 6 26 POTENTIAL.
SQ SEQUENCE 204 AA; 22840 MW; 7B86FA9F125F19BF CRC64;
Query Match 90.3%; Score 28; DB 1; Length 204;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 160 STSNLAS 166
|||||:|

RESULT 2

VLI1_HPV16
ID VLI1_HPV16 STANDARD; PRT; 531 AA.
AC P03101;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Major capsid protein L1.
GN Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE OF 328-371 FROM N.A.
RX MEDLINE=92407963; PubMed=1326639;
RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
variants: a showcase for the molecular evolution of DNA viruses.";
RL J. Virol. 66:5714-5725(1992).
CC -!- MISCELLANEOUS: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE
OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.
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CC EMBL; K02718; AAA46943.1; -;
DR EMBL; M96285; AAA47024.1; -;
DR EMBL; A06331; CAA00546.1; -;
DR PIR; A03640; P1WLHS.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; Late_protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 531 AA; 59554 MW; 5B3402587093B380 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 531;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 308 STANLAS 314

RESULT 3
ID YFK5_SCHPO STANDARD; PRT; 601 AA.
AC P87132;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C167.05 in chromosome I.
GN SPAC167.05 OR SPAC57A7.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouris J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt K., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
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CC
CC EMBL; AL035248; CAA22850.1; -;
DR EMBL; Z95396; CAB08759.1; -;
DR InterPro; IPR000041; Usp.
DR Pfam; PF00582; Usp; 1.
KW Hypothetical protein.
SQ SEQUENCE 601 AA; 65947 MW; 13FACABDCE14239 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 601;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 143 STSNLSS 149

RESULT 4
ID YJ9C_YEAST STANDARD; PRT; 707 AA.
AC P47166;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 81.2 kDa protein in NMD5-HOM6 intergenic region.
GN YJRI34C OR J2120.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO PARAMYOSINS AND MYOSINS.
CC
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DR EMBL; Z49634; CAA89665.1; -.
DR EMBL; Z49635; CAA89667.1; -.
DR SGD; S0003895; YJR134C
KW Hypothetical protein; Coiled coil.
FT DOMAIN 122 473
FT COILED COIL (POTENTIAL).
FT COILED COIL (POTENTIAL).
SQ SEQUENCE 707 AA; 81171 MW; BA47D1A7265BF3D9 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 707;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 25 STSNLS 31

RESULT 5
KV6K_MOUSE
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
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CC -----
DR EMBL; K00746; AAA38691.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT FRAMEWORK-1.
FT DOMAIN 24 33
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48
FT FRAMEWORK-2.
FT DOMAIN 49 55
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87
FT FRAMEWORK-3.
FT DOMAIN 88 98
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 99 108
FT FRAMEWORK-4.
FT DISULFID 23 87
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNLAS 7
Db 50 TSNLAS 55

RESULT 6
YRP2_IRV6
ID YRP2_IRV6 STANDARD; PRT; 126 AA.
AC P18306;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Repetitive protein ORF2.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10486;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=89073753; PubMed=3201751;
RA Fischer M., Schnitzler P., Scholz J., Roesen-Wolff A., Delli H.,
RA Darai G.;
RT "DNA nucleotide sequence analysis of the PvuII DNA fragment L of the
genome of insect iridescent virus type 6 reveals a complex cluster of
multiple tandem, overlapping, and interdigitated repetitive DNA
elements.";
RL Virology 167:497-506(1988).
CC -1- SIMILARITY: A CONSENSUS SEQUENCE MANLX(6)IGSSSTX(6)LX(1)
CC LGSX(1)LOISGX(2)LX(1)VN WAS FOUND IN ALL FIVE ORFS.
CC -----
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CC -----
DR EMBL; M23625; AAA66587.1; -.
DR PIR; B31828; RPXFJ.
KW Hypothetical protein.
FT SIMILAR 1 39
SQ SEQUENCE 126 AA; 13371 MW; 2C927A1D41C41471 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 126;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 15 STSNLS 21

RESULT 7
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
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FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 235 255 POTENTIAL.
SQ SEQUENCE 255 AA; 2760 MW; 7C0936C07F7B58F5 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TSNSLAS 7
Db 185 TSNSLAS 190

RESULT 10
GTSE_HUMAN
ID GTSE_HUMAN STANDARD; PRT; 720 AA.
AC Q9NYZ3; Q9BR20; Q9Y557; Q9UG29;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE G2 and S phase expressed protein 1 (B99 homolog).
GN GTSE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20432105; PubMed=10974554;
RA Monte M., Collavin L., Lazarevic D., Utrera R., Dragani T.A.,
RA Schneider C.;
RT "Cloning, chromosome mapping and functional characterization of a
RL human homologue of murine Gtse-1 (B99) gene.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Leo H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,

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RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in p53-induced cell cycle arrest in G2/M
CC phase by interfering with microtubule rearrangements that are
CC required to enter mitosis. Overexpression delays G2/M phase
CC progression.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.
CC -!- DEVELOPMENTAL STAGE: Expressed in G2/M phase. Not detected in
CC quiescent cells.
CC -!- PTM: Phosphorylated in mitosis (By similarity).
CC -----
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CC -----
DR EMBL; AF223408; AAF31459.1; -
DR EMBL; AL031588; CAB38415.1; -
DR EMBL; AL022325; CAB63079.1; -
DR EMBL; BC006325; AAH06325.1; -
KW Microtubules; Phosphorylation.
FT DOMAIN 22 27 POLY-SER.
FT CONFLICT 259 259 V -> I (IN REF. 1).
FT CONFLICT 506 506 R -> W (IN REF. 2; CAB38415).
SQ SEQUENCE 720 AA; 76614 MW; ACD91CCCD008A89C CRC64;

Query Match 87.1%; Score 27; DB 1; Length 720;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLA 6
Db 303 STSNLA 308

RESULT 11
YB03_YEAST
ID YB03_YEAST STANDARD; PRT; 919 AA.
AC P38073;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative 103.4 kDa transcriptional regulatory protein in RPL4A-HMT1
DE intergenic region.
GN YB033W OR YB0318.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94378725; PubMed=8091864;
RA Smits P.H.M., de Haan M., Maat C., Grivell L.A.;

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"The complete sequence of a 33 kb fragment on the right arm of chromosome II from *Saccharomyces cerevisiae* reveals 16 open reading frames, including ten new open reading frames, five previously identified genes and a homologue of the SCO1 gene.";

Yeast 10:S75-S80(1994).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR

CC CLUSTER DOMAIN.

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 CC -----

DR EMBL: X76078; CAAS3688.1; -;

DR EMBL: Z35902; CAAS4975.1; -;

DR PIR: S45889; S45889.

DR SGD: S0000237; YBR033W.

DR InterPro: IPR001138; Fungi_Trn.

DR Pfam: PF00172; Zn_c1us; 1.

DR SMART: SM00066; GAL4; 1.

DR PROSITE: PS00463; ZN2_CYG_FUNGAL_1; 1.

DR PROSITE: PS50048; ZN2_CYG_FUNGAL_2; 1.

KW Hypothetical protein; Transcription regulation; DNA-binding;

KW Nuclear protein; Zinc; Metal-binding.

FT DNA_BIND 56 85 ZN(2)-CYS(6), FUNGAL-TYPE.

SQ SEQUENCE 919 AA; 103396 MW; 18DD2E37A042E246 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 919;

Best Local Similarity 100.0%; Pred. No. 99;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNIAS 7

Db 756 TSNIAS 761

RESULT 12

KELC_DROME

ID KELC_DROME STANDARD; PRT: 1477 AA.

AC Q04652; Q04653; Q9VJAZ;

DT 01-FEB-1994 (Rel. 28, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ring canal kelch protein [Contains: Kelch short protein].

GN KEL OR CG7210.

OS *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RC MEDLINE=93201592; PubMed=8453663;

RA Xue F., Cooley L.;

RT "Kelch encodes a component of intercellular bridges in *Drosophila* egg

chambers.";

RL Cell 72:681-693(1993).

[2]

RP SEQUENCE FROM N.A.

RC SPRAIN=Berkeley;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Durbin K.K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fostler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Glodek A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.N., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*.";

RL Science 287:2185-2195(2000).

RN [3]

RP CHARACTERIZATION.

RC TISSUE=Embryo;

RC MEDLINE=97236487; PubMed=9118811;

RA Robinson D.N., Cooley L.;

RT "Examination of the function of two kelch proteins generated by stop

codon suppression.";

RL Development 124:1405-1417(1997).

CC -1- FUNCTION: COMPONENT OF RING CANALS THAT REGULATES THE FLOW OF

CYTOPLASM BETWEEN CELLS. MAY BE INVOLVED IN THE REGULATION OF

CYTOPLASM FLOW FROM NURSE CELLS TO THE OOCYTE DURING OOGENESIS.

CC BINDS ACTIN.

CC -1- SUBCELLULAR LOCATION: INNER SURFACE OF CYTOPLASMIC BRIDGES OR RING

CANALS PRESENT IN EGG CHAMBERS. SUBCORTICALLY IN IMAGINAL DISK

EPITHELIA.

CC -1- TISSUE SPECIFICITY: BOTH PROTEINS ARE EXPRESSED IN OVARIES, MALE

IMAGINAL DISKS. KELCH ORF1 IS THE PREDOMINANT PROTEIN AND IS ALSO

EXPRESSED IN FAT BODIES. ON ENTRY INTO METAMORPHOSIS LEVELS OF

FULL LENGTH PROTEIN INCREASE IN TESTIS AND IMAGINAL DISKS.

CC -1- DEVELOPMENTAL STAGE: LARVAE, PUPAE AND ADULTS.

CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.

CC -1- SIMILARITY: CONTAINS 6 KELCH REPEATS.

CC -1- CAUTION: REF.3 BELIEVES RESIDUE 690 IS A SELENOCYSTEINE.

CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous

gene model prediction.

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DR EMBL: L08483; AAA53471.1; -;

DR EMBL: L08483; AAA53472.2; -;

DR EMBL: AE003657; AAF53651.1; ALT_SEQ.

DR HSSP: Q05516; 1CS3.

DR FlyBase: FBgn0001301; kel.

DR InterPro: IPR000210; BTB_POZ.

DR InterPro: IPR001798; Kelch.

Query Match 83.9%; Score 26; DB 1; Length 87;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 5 STSDLAS 11

RESULT 14
SP12_YEAST STANDARD; PRT; 173 AA.

ID SP12_YEAST
AC P17123;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sporulation protein SP012.
GN SP012 OR YHR152W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90258869; Pubmed=2188099;
RA Malavasic M.J., Elder R.T.;
RT "Complementary transcripts from two genes necessary for normal
RT meiosis in the yeast Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 10:2809-2819(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c/AB972;
RX JOHNSON M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
CC -!- FUNCTION: IT IS REQUIRED FOR MEIOSIS I CHROMOSOME DIVISION DURING
CC SPORULATION.
CC -!- MISCELLANEOUS: ITS NEGATIVE TAIL IS FUNCTIONALLY IMPORTANT.
CC -!- SIMILARITY: TO YEAST G8558.
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CC -----
CC EMBL; M32653; AAA35076.1;
CC EMBL; U10397; AAB68979.1;
CC PIR; B36321; B36321.
CC PIR; S46756; S46756.
CC SGD; S0001195; SP012.
CC Sporulation; Meiosis.
KW DOMAIN 159 173 NEGATIVE-CHARGED TAIL.
FT SEQUENCE 173 AA; 19912 MW; E114394516451f60 CRC64;
SQ

Query Match 83.9%; Score 26; DB 1; Length 173;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 78 STSNLAS 84

RESULT 13
IM08_YEAST
ID IM08_YEAST STANDARD; PRT; 87 AA.
AC P57744;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM8.
GN TIM8 OR YJRL35W-A OR YJRL35BW.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBDJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -----
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CC -----
CC EMBL; Z49636; -; NOT_ANNOTATED_CDS.
CC SGD; S0007348; TIM8.
CC InterPro: IPR004217; Znf_Tim10/DDP.
CC Pfam; PF02953; zf-Tim10_DDP; 1.
KW Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
SQ SEQUENCE 87 AA; 9764 MW; B91D1DDA1707EA24 CRC64;
SQ

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RESULT 15
E13B_HORVU
ID E13B_HORVU STANDARD; PRT; 334 AA.
AC P15737;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucan endo-1,3-beta-glucosidase GII precursor (EC 3.2.1.39) ((1->3)-
DE beta-glucan endohydrolase GII) ((1->3)-beta-glucanase isoenzyme GII)
DE (Beta-1,3-endoglucanase GII).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-68.
RC STRAIN=cv. Clipper;
RX MEDLINE=93357431; PubMed=2562758;
RA Hoej P.B., Hartman D.J., Morrice N.A., Doan D.N.P., Fincher G.B.;
RT "Purification of (1->3)-beta-glucan endohydrolase isoenzyme II from
RT germinated barley and determination of its primary structure from a
RT cDNA clone.";
RL Plant Mol. Biol. 13:31-42(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Piggy;
RX MEDLINE=91107649; PubMed=1899089;
RA Leah R., Tommerup H., Svendsen I., Mundy J.;
RT "Biochemical and molecular characterization of three barley seed
RT proteins with antifungal properties.";
RL J. Biol. Chem. 266:1564-1573(1991).
RN [3]
RP SEQUENCE OF 258-332 FROM N.A.
RC TISSUE=Leaf;
RA Jutidamrongphan W., Mackinnon G., Manners J., Simpson R.S.,
RA Scott K.J.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 29-334.
RA Ballance G.M., Svendsen I.;
RT "Purification and amino acid sequence determination of an endo-1,3-
RT beta-glucanase from barley.";
RL Carlsberg Res. Commun. 53:411-419(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=94195828; PubMed=8146192;
RA Varghese J.N., Garrett T.P.J., Colman P.M., Chen L., Hoej P.B.,
RA Fincher G.B.;
RT "Three-dimensional structures of two plant beta-glucan endohydrolases
RT with distinct substrate specificities.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2785-2789(1994).
CC -1- FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL
CC INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE
CC FUNGAL CELL WALL POLYSACCHARIDES.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC -1- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62907; AAA32939.1; -
DR EMBL; X16274; CAA34350.1; -
DR EMBL; M23548; AAA32958.1; -
DR PIR; S05510; S05510.
DR PIR; A31800; A31800.

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DR PDB; 1GHS; 01-NOV-94.
DR InterPro; IPR000490; Glyco_hydro_17.
DR Pfam; PF00332; Glyco_hydro_17; 1.
DR PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
KW Hydrolase; Glycosidase; Signal; Multigene family; 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 334 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GII.
FT ACT_SITE 259 259 NUCLEOPHILE.
FT ACT_SITE 316 316 PROTON DONOR.
FT CONFLICT 12 12 A -> V (IN REF. 2).
FT CONFLICT 71 71 L -> V (IN REF. 2).
SQ SEQUENCE 334 AA; 35193 MW; 552D66A29A08C703 CRC64;
Query Match 83.9%; Score 26; DB 1; Length 334;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 93 STSNAAS 99

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Search completed: December 23, 2002, 07:26:08
Job time : 2.69186 secs

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OM protein - protein search, using sw model

Run On: December 23, 2002, 07:17:27 : Search time 2.9031 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	31	100.0	265 16 Q8YDZ0	Q8YDZ0 brucella me
2	31	100.0	388 2 Q9KIS6	Q9KIS6 brucella ab
3	31	100.0	391 2 Q9RPX5	Q9RPX5 brucella su
4	31	100.0	595 9 Q37901	Q37901 bacterioph
5	31	100.0	753 5 Q26306	Q26306 drosophila
6	31	100.0	1107 3 Q12271	Q12271 saccharomyc
7	28	90.3	97 11 Q9JL76	Q9JL76 mus musculu
8	28	90.3	187 10 Q9C5K8	Q9C5K8 arabidopsis
9	28	90.3	401 3 Q8X084	Q8X084 neurospora
10	28	90.3	494 12 Q80996	Q80996 human papil
11	28	90.3	494 12 Q80997	Q80997 human papil
12	28	90.3	494 12 Q80998	Q80998 human papil
13	28	90.3	494 12 Q80999	Q80999 human papil
14	28	90.3	494 12 Q81000	Q81000 human papil
15	28	90.3	494 12 Q81001	Q81001 human papil
16	28	90.3	494 12 Q81002	Q81002 human papil

17	28	90.3	494	12	Q81004	Q81004 human papil
18	28	90.3	494	12	Q81005	Q81005 human papil
19	28	90.3	494	12	Q81006	Q81006 human papil
20	28	90.3	494	12	Q81007	Q81007 human papil
21	28	90.3	494	12	Q81008	Q81008 human papil
22	28	90.3	494	12	Q81009	Q81009 human papil
23	28	90.3	494	12	Q81010	Q81010 human papil
24	28	90.3	494	12	Q81011	Q81011 human papil
25	28	90.3	494	12	Q81012	Q81012 human papil
26	28	90.3	494	12	Q90204	Q90204 human papil
27	28	90.3	495	12	Q12343	Q12343 human papil
28	28	90.3	505	12	Q9WLQ5	Q9WLQ5 human papil
29	28	90.3	505	12	Q92282	Q92282 human papil
30	28	90.3	505	12	Q9WHS5	Q9WHS5 human papil
31	28	90.3	505	12	Q9WHS6	Q9WHS6 human papil
32	28	90.3	505	12	Q9WPH4	Q9WPH4 human papil
33	28	90.3	505	12	Q9WLQ6	Q9WLQ6 human papil
34	28	90.3	522	3	Q96VF4	Q96VF4 uromyces fa
35	28	90.3	531	12	Q00530	Q00530 human papil
36	28	90.3	531	16	Q8Z0P3	Q8Z0P3 anabaena sp
37	28	90.3	567	3	P78871	P78871 schizosacch
38	28	90.3	597	16	Q9PPX0	Q9PPX0 ureaplasma
39	28	90.3	963	16	O07232	O07232 mycobacteri
40	28	90.3	1026	5	Q961S4	Q961S4 drosophila
41	28	90.3	1333	5	Q24262	Q24262 drosophila
42	28	90.3	3186	16	Q8VKN2	Q8VKN2 mycobacteri
43	27	87.1	101	11	Q9JL78	Q9JL78 mus musculu
44	27	87.1	106	5	Q9U410	Q9U410 schistosoma
45	27	87.1	135	5	Q95275	Q95275 oostertagia

ALIGNMENTS

RESULT 1

Q8YDZ0 PRELIMINARY; PRT; 265 AA.
AC Q8YDZ0:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Channel protein VIRB10 homolog.
GN BMEI10034.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009642; AAL53275.1; -.
KW Complete proteome.
SQ SEQUENCE 265 AA; 28204 MW; 042033AA2FD5EC73 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 219 STSNLAS 225

RESULT 2

Q9KIS6
ID Q9KIS6 PRELIMINARY; PRT; 388 AA.
DE Q9KIS6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-DEC-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VirB10.
GN VIRB10.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RX MEDLINE=20398168; PubMed=10940027;
RA Steira R.; Comerici D.J.; Sanchez D.O.; Ugalde R.A.;
RT "A Homologue of an Operon Required for DNA Transfer in Agrobacterium
RT Is Required in Brucella abortus for Virulence and Intracellular
RT Multiplication."
RL J. Bacteriol. 182:4849-4855(2000).
DR EMBL; AF226278; AAF73903.1;
SQ SEQUENCE 388 AA; 41193 MW; D8A63372B267E7F3 CRC64;
Query Match 100.0%; Score 31; DB 2; Length 388;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 342 STSNLAS 348
RESULT 3
Q9RFX5
ID Q9RFX5 PRELIMINARY; PRT; 391 AA.
AC Q9RFX5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VirB10.
GN VIRB10.
OS Brucella suis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330;
RX MEDLINE=99440171; PubMed=10510235;
RA O'Callaghan D.; Cazeville C.; Allardet-Servent A.; Boschioli M.L.;
RA Bourg G.; Foulongne V.; Frutos P.; Kulakov Y.; Ramuz M.;
RT "A homologue of the Agrobacterium tumefaciens VirB and Bordetella
RT pertussis Ptl type IV secretion systems is essential for intracellular
RT survival of Brucella suis."
RL Mol. Microbiol. 33:1210-1220(1999).
DR EMBL; AF141604; ARD56620.1;
SQ SEQUENCE 391 AA; 41453 MW; A6DCA4C9AFBB490D CRC64;
Query Match 100.0%; Score 31; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 345 STSNLAS 351
RESULT 4
Q37901
ID Q37901 PRELIMINARY; PRT; 595 AA.
AC Q37901
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tail protein.
DE HRS.
GN Bacteriophage BF23.
OS Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC T5-like viruses.
OX NCBI_TaxID=10707;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96204568; PubMed=86233528;
RA Mendigler M.; Holz T.; Heller K.J.;
RT "Identification of the receptor-binding regions of pb5 proteins of
RT bacteriophages T5 and BF23."
RL Virology 219:19-28(1996).
DR EMBL; L42820; AAB05216.1;
SQ SEQUENCE 595 AA; 63909 MW; E79B717F88EA2099 CRC64;
Query Match 100.0%; Score 31; DB 9; Length 595;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 264 STSNLAS 270
RESULT 5
Q26306
ID Q26306 PRELIMINARY; PRT; 753 AA.
AC Q26306;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEU-NEURALIZED.
GN NEUR OR NEU OR CG11988.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93285130; PubMed=8508781;
RA Boulianne G.L.; la Concha A.; Campos-Ortega J.A.; Jan L.Y.; Jan Y.N.;
RT "The Drosophila neurogenic gene neuralized encodes a novel protein and
RT is expressed in precursors of larval and adult neurons."
RL EMBO J. 12:2586-2586(1993).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; S62597; AAB27151.1;
DR FlyBase; FBgn002932; neur.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 753 AA; 82307 MW; 45056A93EDDA7B41 CRC64;
Query Match 100.0%; Score 31; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 585 STSNLAS 591
RESULT 6
Q12271
ID Q12271 PRELIMINARY; PRT; 1107 AA.
AC Q12271;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE YOR3231W from chromosome XV.
GN INF53 OR YOR3231W OR YOR109W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Andrade M.A., Rechmann S., Teodoru C., Banrevi A.,
RA Sander C., Valencia A., Ansoorge W., Voss H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Voss H., Benes V., Rechmann S., Teodoru C., Schwager C., Paces V.,
RA Ansoorge W.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94335; CAA64029.1; -;
DR EMBL; Z75017; CAA99307.1; -;
DR SGD; S0005635; INP53.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000300; IPPc.
DR InterPro; IPR002013; Syja_N.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF02383; Syja_N; 1.
DR SMART; SM00128; IPPc; 1.
SQ SEQUENCE 1107 AA; 124576 MW; 1E024F15085261EA CRC64;
Query Match 100.0%; Score 31; DB 3; Length 1107;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
DB 1029 STSNLAS 1035
RESULT 7
QJUL76
ID Q9JUL76 PRELIMINARY; PRT; 97 AA.
AC Q9JUL76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-mysin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -;
DR HSP; P01679; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9E1FFE1F49DA1C CRC64;
Query Match 90.3%; Score 28; DB 11; Length 97;

Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
DB 39 ATSNLAS 45
RESULT 8
Q9C5K8
ID Q9C5K8 PRELIMINARY; PRT; 187 AA.
AC Q9C5K8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 19.9 kDa protein.
GN F22D1.70/AT5G20900.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene F22D1.70/AT5G20900";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers W.C., Miranda M., Narusaka M., Narusaka M., Nguyen M.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene F22D1.70/AT5G20900";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360184; AAK25894.1; -;
DR EMBL; AY051013; AAK93690.1; -;
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 19933 MW; 4F0C66DECB4F0E1 CRC64;
Query Match 90.3%; Score 28; DB 10; Length 187;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
DB 112 STSNVAS 118
RESULT 9
Q8X084
ID Q8X084 PRELIMINARY; PRT; 401 AA.
AC Q8X084;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Related to vegetative cell wall protein gpl.
GN B14D6.440.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.

DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1 494
SQ SEQUENCE 494 AA; 55021 MW; E446FD38994FB3DD CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
||:||||
DB 273 STANLAS 279

RESULT 13
Q80999 PRELIMINARY; PRT; 494 AA.
AC Q80999;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NM T455;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NM T455;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34169; AAA91716.1; -.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_Capsid_L1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1 494
SQ SEQUENCE 494 AA; 55051 MW; 8DE5FC4CCD7DE5D8 CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
||:||||
DB 273 STANLAS 279

RESULT 14
Q81000 PRELIMINARY; PRT; 494 AA.
AC Q81000;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;

RN SEQUENCE FROM N.A.
RP STRAIN-NM T529;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NM T529;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34170; AAA91717.1; -.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_Capsid_L1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1 494
SQ SEQUENCE 494 AA; 55063 MW; 735F7C2B86CAC58F CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
||:||||
DB 273 STANLAS 279

RESULT 15
Q81001 PRELIMINARY; PRT; 494 AA.
AC Q81001;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Late major capsid protein L1 (fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OR 1905;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OR 1905;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34172; AAA91719.1; -.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_Capsid_L1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1 494
SQ SEQUENCE 494 AA; 55094 MW; ECB31B09E8EFB4E3 CRC64;

Query Match 90.3%; Score 28; DB 12; Length 494;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STSNLAS 7
 ||:||||
Db 273 STANLAS 279

Search completed: December 23, 2002, 07:29:52
Job time : 4.9031 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: Decemb4r 23, 2002, 07:20:23 : Search time 1.62209 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	93.8	9	2	US-08-116-778E-11
2	45	93.8	9	2	US-08-438-562-11
3	45	93.8	9	2	US-08-483-528B-99
4	45	93.8	9	4	US-09-393-385B-110
5	45	93.8	129	2	US-08-116-778E-2
6	45	93.8	129	2	US-08-438-562-2
7	45	93.8	129	2	US-08-483-528B-92
8	45	93.8	130	4	US-09-393-385B-111
9	45	93.8	130	4	US-09-393-385B-113
10	45	93.8	133	2	US-08-116-778E-37
11	45	93.8	133	2	US-08-438-562-37
12	45	93.8	133	2	US-08-483-528B-101
13	42	87.5	270	2	US-08-652-507-2
14	42	87.5	553	2	US-08-661-052-16
15	42	87.5	553	4	US-09-188-082-16
16	42	87.5	553	4	US-09-364-088-16
17	42	87.5	553	4	US-09-102-716-16
18	39	81.2	9	4	US-09-171-945-28
19	39	81.2	107	4	US-09-171-945-50
20	39	81.2	107	4	US-09-171-945-61
21	39	81.2	107	4	US-09-171-945-65
22	39	81.2	107	4	US-09-171-945-71
23	39	81.2	108	4	US-09-171-945-9
24	39	81.2	235	4	US-09-171-945-17
25	39	81.2	235	4	US-09-171-945-52
26	39	81.2	235	4	US-09-171-945-97
27	39	81.2	235	4	US-09-171-945-99

28	39	81.2	281	4	US-09-423-439-44	Sequence 44, Appl
29	39	81.2	666	4	US-09-423-439-51	Sequence 51, Appl
30	38	79.2	108	2	US-08-378-939-32	Sequence 32, Appl
31	38	79.2	108	2	US-08-378-939-34	Sequence 34, Appl
32	37	77.1	105	3	US-08-434-000A-12	Sequence 12, Appl
33	37	77.1	105	4	US-09-312-157-12	Sequence 12, Appl
34	37	77.1	230	4	US-09-485-737B-102	Sequence 102, Appl
35	37	77.1	233	4	US-09-485-737B-69	Sequence 69, Appl
36	37	77.1	235	4	US-09-485-737B-93	Sequence 93, Appl
37	37	77.1	240	4	US-09-485-737B-91	Sequence 91, Appl
38	37	77.1	267	4	US-09-485-737B-2	Sequence 2, Appl
39	37	77.1	541	4	US-09-485-737B-85	Sequence 85, Appl
40	37	77.1	711	4	US-09-485-737B-90	Sequence 90, Appl
41	36	75.0	108	4	US-09-157-370-4	Sequence 4, Appl
42	36	75.0	130	2	US-08-659-567-2	Sequence 2, Appl
43	36	75.0	249	2	US-08-797-689-18	Sequence 18, Appl
44	35	72.9	107	3	US-08-554-840-1	Sequence 1, Appl
45	35	72.9	107	3	US-08-554-840-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-116-778E-11
; Sequence 11, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-778E-11

Query Match 93.8%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
|||||||

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-393-385B-110

Query Match 93.8%; Score 45; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9
| | | | | | | | | |
Db 1 QORSSYPPT 9

RESULT 5

US-08-116-778E-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470

GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KIWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-SEP-93
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: sig_peptide
LOCATION: -22...-1

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS

FEATURE:

NAME/KEY: domain
LOCATION: 24..33

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS

OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"

FEATURE:

NAME/KEY: domain
LOCATION: 49..55

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS

;
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:

NAME/KEY: domain
LOCATION: 88..96

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS

; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"

US-08-116-778E-2

Query Match 93.8%; Score 45; DB 2; Length 129;

Best Local Similarity 88.9%; Pred. No. 0.12;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9
| | | | | | | | | |

Db 110 QORSSYPPT 118

RESULT 6

US-08-438-562-2
; Sequence 2, Application US/08438562
; Patent No. 5874255

GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KIWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-95
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: sig_peptide
LOCATION: -22...-1

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS

FEATURE:

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; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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US-08-438-562-2
Query Match 93.8%; Score 45; DB 2; Length 129;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
    |||||
Db 110 QORSSYPPT 118

RESULT 7
US-08-483-528B-92
; Sequence 92: Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNANA, YOSHIIISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4100
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD:

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; IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO AN
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
;
US-08-483-528B-92
Query Match 93.8%; Score 45; DB 2; Length 129;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
    |||||
Db 110 QORSSYPPT 118

RESULT 8
US-09-393-385B-111
; Sequence 111, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNANA, YOSHIIISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-393-385B-I11

Query Match 93.8%; Score 45; DB 4; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|11111111|
Db 110 QORSSYPPT 118

RESULT 9

US-09-393-385B-113
; Sequence 113, Application US/09393385B
; Patent No. 6423511

; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96

; CLASSIFICATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-393-385B-113

Query Match 93.8%; Score 45; DB 4; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|11111111|
Db 110 QORSSYPPT 118

RESULT 10

US-08-116-778E-37
; Sequence 37, Application US/08116778E
; Patent No. 5830470

; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES

; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-116-778E-37

Query Match 93.8%; Score 45; DB 2; Length 133;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|11111111|
Db 110 QORSSYPPT 118

RESULT 11

US-08-438-562-37
; Sequence 37, Application US/08438562
; Patent No. 5874255

; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-562-37

Query Match 93.8%; Score 45; DB 2; Length 133;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9
|||||||
Db 110 QORSSYPPT 118

RESULT 12
US-08-483-528B-101
Sequence 101, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUNANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-528B-101

Query Match 93.8%; Score 45; DB 2; Length 133;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9
|||||||
Db 110 QORSSYPPT 118

RESULT 13
US-08-652-507-2
Sequence 2, Application US/08652507
Patent No. 5876691
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhve, P.C.
STREET: 1100 No. 5876691th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-2

Query Match 87.5%; Score 42; DB 2; Length 270;
Best Local Similarity 88.9%; Pred. No. 0.92;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9
|||||||
Db 249 QORSSYPPT 257

RESULT 14
US-08-661-052-16
Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-16

Query Match 87.5%; Score 42; DB 2; Length 553;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
DB 499 QORSSYPLT 507

RESULT 15
US-09-188-082-16
Sequence 16, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-188-082-16

Query Match 87.5%; Score 42; DB 4; Length 553;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
DB 499 QORSSYPLT 507

Search completed: December 23, 2002, 07:33:15
Job time : 2.62209 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 0.837209 seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-6

Perfect score: 48

Sequence: 1 QORSSYPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	10	US-09-976-787-6
2	48	100.0	9	10	US-09-865-198-6
3	48	100.0	106	10	US-09-976-787-24
4	48	100.0	106	10	US-09-865-198-23
5	48	100.0	108	10	US-09-976-787-8
6	48	100.0	108	10	US-09-865-198-8
7	48	100.0	131	10	US-09-881-823-6
8	48	100.0	238	10	US-09-976-787-29
9	48	100.0	238	10	US-09-865-198-28
10	48	100.0	240	10	US-09-976-787-28
11	48	100.0	240	10	US-09-865-198-27
12	45	93.8	107	9	US-09-144-886-88
13	45	93.8	112	9	US-09-144-886-89
14	43	89.6	9	10	US-09-808-037-17
15	43	89.6	9	10	US-09-808-037-19
16	43	89.6	119	10	US-09-808-037-28
17	43	89.6	239	10	US-09-808-037-6
18	40	83.3	9	10	US-09-808-037-18
19	40	83.3	107	9	US-09-144-886-75

Sequence 28, Appl
Sequence 50, Appl
Sequence 61, Appl
Sequence 65, Appl
Sequence 71, Appl
Sequence 9, Appl
Sequence 17, Appl
Sequence 52, Appl
Sequence 97, Appl
Sequence 99, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 18, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 20, Appl
Sequence 78, Appl
Sequence 79, Appl
Sequence 96, Appl
Sequence 1076, Ap
Sequence 5, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 51, Appl
Sequence 80, Appl
Sequence 2, Appl

39 81.2 9 10 US-09-910-059-28
39 81.2 107 10 US-09-910-059-50
39 81.2 107 10 US-09-910-059-61
39 81.2 107 10 US-09-910-059-65
39 81.2 107 10 US-09-910-059-71
39 81.2 108 10 US-09-910-059-9
39 81.2 235 10 US-09-910-059-17
39 81.2 235 10 US-09-910-059-52
39 81.2 235 10 US-09-910-059-97
39 81.2 235 10 US-09-910-059-99
37 77.1 105 9 US-09-982-107-12
37 77.1 669 9 US-09-807-721-2
32 36 75.0 249 10 US-09-984-186-18
33 35 72.9 9 10 US-09-808-037-15
34 35 72.9 9 10 US-09-808-037-16
35 35 72.9 9 10 US-09-808-037-20
36 34 70.8 107 9 US-09-144-886-78
37 34 70.8 109 9 US-09-144-886-79
38 34 70.8 109 9 US-09-144-886-96
39 33 68.8 53 10 US-09-867-550-1076
40 32 66.7 9 9 US-09-771-415-5
41 32 66.7 9 9 US-09-996-288-6
42 32 66.7 9 10 US-09-796-848A-7
43 32 66.7 9 10 US-09-828-708-51
44 32 66.7 102 10 US-09-905-243-80
45 32 66.7 104 10 US-09-828-708-2

ALIGNMENTS

RESULT 1
US-09-976-787-6
; Sequence 6, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-976-787-6

Query Match 100.0%; Score 48; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
Db 1 QORSSYPFT 9

RESULT 2
US-09-865-198-6
; Sequence 6, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-6

Query Match 100.0%; Score 48; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
Db 1 QORSSYPFT 9

RESULT 3
US-09-976-787-24

; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 4
US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 5
US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 6
US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 7
US-09-881-823-6

; Sequence 6, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-6

Query Match 100.0%; Score 48; DB 10; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
| | | | | | | | | |
Db 110 QORSSYPFT 118

RESULT 8

; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
| | | | | | | | | |
Db 220 QORSSYPFT 228

RESULT 9

; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102

; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
| | | | | | | | | |
Db 220 QORSSYPFT 228

RESULT 10

; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
| | | | | | | | | |
Db 220 QORSSYPFT 228

RESULT 11

; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match 100.0%; Score 48; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||N|||

Db 220 QORSSYPPT 228

RESULT 12

US-09-144-886-88
; Sequence 88; Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: Botulinum Neurotoxins
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bont/a clone
US-09-144-886-88

Query Match 93.8%; Score 45; DB 9; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||N|||

Db 88 QORSSYPPT 96

RESULT 13

US-09-144-886-89
; Sequence 89; Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: Botulinum Neurotoxins
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bont/a clone
US-09-144-886-89

Query Match 93.8%; Score 45; DB 9; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||N|||

Db 93 QORSSYPPT 101

RESULT 14

US-09-808-037-17
; Sequence 17; Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-17

Query Match 89.6%; Score 43; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QORSSYPPT 9
|||||N|||

Db 2 QORSSYPPT 9

RESULT 15

US-09-808-037-19
; Sequence 19; Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-19

Query Match 89.6%; Score 43; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QORSSYPPT 9
|||||N|||

Db 2 QORSSYPPT 9

Search completed: December 23, 2002, 07:58:19
Job time : 0.837209 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 0.889535 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QORSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	77.1	1501	1 NINC_DROME	P10676 drosophila
2	35	72.9	108	1 KVLV_HUMAN	P04430 homo sapien
3	34	70.8	108	1 KVL1_CANFA	P01618 canis famil
4	34	70.8	275	1 CHRL_VIBCH	O9kq06 vibrio chol
5	34	70.8	341	1 HEAD_LAMBD	P03713 bacterioph
6	34	70.8	343	1 CYSL_DICDI	P04988 dictyosteli
7	33	68.8	108	1 KVL1_HUMAN	P01604 homo sapien
8	33	68.8	345	1 YDE9_SCHPO	Q10442 schizosacch
9	33	68.8	556	1 PPBD_BACSU	P42251 bacillus su
10	33	68.8	662	1 YLN9_CAEEL	Q09512 caenorhabdi
11	32	66.7	265	1 TF2D_STRPU	P91809 strongyloce
12	32	66.7	446	1 CN7B_MOUSE	O9qx91 mus musculu
13	32	66.7	450	1 CN7B_HUMAN	O9np56 homo sapien
14	32	66.7	872	1 SCD5_YEAST	P34758 saccharomyc
15	32	66.7	1476	1 A77A_CRIGR	P49015 cricetus
16	31	64.6	129	1 KVL4_MOUSE	P01680 mus musculu
17	31	64.6	275	1 CHER_VIBAN	O57508 vibrio angu
18	31	64.6	275	1 CHER_VIBPA	O9x9k2 vibrio para
19	31	64.6	360	1 CHLI_MESVI	Q9mut3 mesostigma
20	31	64.6	398	1 KTEL_KLULA	P40952 kluyveromyc
21	31	64.6	588	1 CMC2_CAEEL	Q20799 caenorhabdi
22	31	64.6	673	1 FXO3_HUMAN	O43524 homo sapien
23	31	64.6	750	1 PTP2_YEAST	P29461 saccharomyc
24	31	64.6	891	1 MAZ3_SCHCO	P37937 schizophyll
25	31	64.6	1115	1 D3PA_BACSU	O34623 bacillus su
26	30	62.5	118	1 YMX2_YEAST	Q04276 saccharomyc
27	30	62.5	268	1 Y145_METJA	Q57609 methanococc
28	30	62.5	313	1 VU47_HSV7J	P52525 human herpe
29	30	62.5	317	1 YRC3_CAEEL	Q10042 caenorhabdi
30	30	62.5	329	1 YHO3_YEAST	P14693 saccharomyc
31	30	62.5	376	1 CYS2_DICDI	P04989 dictyosteli
32	30	62.5	380	1 CYB_HUMAN	P00156 homo sapien
33	30	62.5	396	1 REPA_BACSU	P13962 bacillus su

RESULT 1
NINC_DROME
ID NINC_DROME STANDARD; PRT; 1501 AA.
AC P10676; P10677;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neither inactivation nor afterpotential protein C (EC 2.7.1.37).
GN NINAC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RA MEDLINE=88151067; PubMed=2449973;
RX Montell C., Rubin G.M.;
RT "The Drosophila ninac locus encodes two photoreceptor cell specific
proteins with domains homologous to protein kinases and the myosin
heavy chain head."
RL Cell 52:757-772(1988).
CC -!- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC
PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN
ACTIVITIES.
CC -!- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: CYTOSKELETON.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
short form; are produced by alternative splicing.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SER/THR
FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN
SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; J03131; AAA28718.1; -
CC EMBL; J03131; AAA28719.1; -
CC EMBL; M20230; AAA28721.1; -
CC EMBL; M20231; AAA28720.1; -
CC PIR; A29813; A29813.
CC PIR; B29813; B29813.
CC HSSP; P08799; 1MND.
CC FlyBase; FBgn0002938; ninac.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR000048; IQ_region.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR001609; myosin_head.
CC Pfam; PF00063; myosin_head; 1.

ALIGNMENTS

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DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00612; IQ; 2.
DR ProDom: PB000001; Euk_pkinase; 1.
DR ProDom: PB000355; myosin_head; 1.
DR SMART: SM00015; IQ; 2.
DR PROSITE: PS00096; IQ; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Cytoskeleton; Actin-binding; ATP-binding; Myosin; Transferase; Vision;
KW Serine/threonine-protein kinase; Alternative splicing.
FT DOMAIN 16 282
FT DOMAIN 335 1035
FT DOMAIN 1036 1065
FT DOMAIN 1066 1501
FT NP_BIND 22 30
FT BINDING 45 45
FT ACT_SITE 145 145
FT DOMAIN 913 934
FT VARSPLIC 1082 1135
FT VARSPLIC 1136 1501
FT CONFLICT 253 253
FT CONFLICT 1089 1089
SQ SEQUENCE 1501 AA; 174269 MW; D167EABC82A3933A CRC64;

Query Match: 77.1%; Score 37; DB 1; Length 1501;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYP 7
DB 1352 QORSSYP 1358

RESULT 2
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region BAN.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dweulet E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR: A01878; KIHUBN.
DR HSPP: P80362; IWTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region; Amyloid.
KW DOMAIN 1 23
KW DOMAIN 24 34
KW DOMAIN 35 49
KW DOMAIN 50 56
KW DOMAIN 57 88
KW DOMAIN 89 97
KW DOMAIN 98 107
KW DISULFID 23 88
KW NON_TER 108 108
KW SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match: 77.1%; Score 37; DB 1; Length 1501;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYP 7
DB 1352 QORSSYP 1358

RESULT 2
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region BAN.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dweulet E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR: A01878; KIHUBN.
DR HSPP: P80362; IWTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region; Amyloid.
KW DOMAIN 1 23
KW DOMAIN 24 34
KW DOMAIN 35 49
KW DOMAIN 50 56
KW DOMAIN 57 88
KW DOMAIN 89 97
KW DOMAIN 98 107
KW DISULFID 23 88
KW NON_TER 108 108
KW SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
```

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Query Match: 72.9%; Score 35; DB 1; Length 108;
Best Local Similarity 56.7%; Pred. No. 2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYP 9
DB 89 QORSSYP 97

RESULT 3
KVL_CANFA
ID KVL_CANFA STANDARD; PRT; 108 AA.
AC P01618;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region GOM.
DE Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
canine myeloma immunoglobulin: evidence that the VK subgroups
predated mammalian speciation.";
RL Immunohemistry 15:303-305(1978).
CC -1- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR: A01907; K2DGM.
DR HSPP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
KW DOMAIN 24 34
KW DOMAIN 35 49
KW DOMAIN 50 56
KW DOMAIN 57 88
KW DOMAIN 89 97
KW DOMAIN 98 107
KW DISULFID 23 88
KW NON_TER 108 108
KW SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match: 70.8%; Score 34; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 3.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QORSSYP 9
DB 90 QORSSYP 97

RESULT 4
CHRL_VIBCH
ID CHRL_VIBCH STANDARD; PRT; 275 AA.
AC O9KQ06; O9XCL5.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chemotaxis protein methyltransferase 1 (EC 2.1.1.80).
GN CHER1 OR CHER OR VC2201.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=EL Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
RA McDaniel L., Utlback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN [2]
RP SEQUENCE OF 10-366 FROM N.A.
RC STRAIN=CVDL10;
RX MEDLINE=99328977; PubMed=10400589;
RA O'Toole R., Lundberg S., Fredriksson S.A., Jansson A., Nilsson B.,
RA Wolf-Watz H.;
RT "The chemotactic response of Vibrio anguillarum to fish intestinal
RT mucus is mediated by a combination of multiple mucus components.";
RL J. Bacteriol. 181:4308-4317(1999).
CC -!- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER
CC RESIDUES IN MCP (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
CC = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC -!- SIMILARITY: CONTAINS 1 CHER-TYPE METHYLTRANSFERASE DOMAIN.
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CC -----
DR EMBL; AE004291; AAF95346.1; -
DR EMBL; AF139167; AAD45254.1; -
DR HSSP; P07801; 1AF7.
DR TIGR; VC2201; -
DR InterPro; IPR000780; ChEr_Metranf.
DR InterPro; IPR001601; Methyltransf.
DR Pfam; PF01739; ChEr; 1.
DR Pfam; PF03705; ChEr_N; 1.
DR PRINTS; PR00996; CHERMTFRASE.
DR SMART; SM00138; MetTC; 1.
DR PROSITE; PS50123; CHER; 1.
KW Transferase; Methyltransferase; Complete proteome.
FT DOMAIN 1 275 CHER-TYPE METHYLTRANSFERASE.
SQ SEQUENCE 275 AA; 30871 MW; F008ADCBFA46A921 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 275;
Best Local Similarity 85.7%; Pred. No. 8.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPT 9
DB 82 RDSYPT 88

RESULT 5
HEAD_LAMBDA STANDARD; PRT; 341 AA.
ID HEAD_LAMBDA
AC P03713;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Major head protein (GPE) (Major coat protein).
GN E.
OS Bacteriophage lambda.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.

SEQUENCE FROM N.A.
[1]
RX MEDLINE=83189071; PubMed=6221115;
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RT "Nucleotide sequence of bacteriophage lambda DNA.";
RL J. Mol. Biol. 162:729-773(1982).
CC -!- FUNCTION: GENE E PROTEIN IS A MAJOR COMPONENT OF THE PHAGE HEAD.
CC THERE ARE ABOUT 420 COPIES OF PROTEIN E PER MATURE PHAGE. SOME OF
CC THE E PROTEIN IS COVALENTLY LINKED WITH AN EQUI-MOLAR AMOUNT OF
CC PROTEIN C AND CLEAVED TO YIELD MINOR CAPSID PROTEINS XI AND X2.
CC -!- SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF PHI-80 AND P21.
CC -----
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CC -----
DR EMBL; J02459; AAA96540.1; -
DR PIR; A04335; VHBPEL.
KW Coat protein.
SQ SEQUENCE 341 AA; 38188 MW; 31C50E4B38DA44A9 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 341;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPT 9
DB 29 RESYPT 35

RESULT 6
CYSL_DICDI STANDARD; PRT; 343 AA.
ID CYSL_DICDI
AC P04988;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine proteinase 1 precursor (EC 3.4.22.-).
GN CPRA OR CPl.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85257519; PubMed=2990918;
RA Williams J.G., North M.J., Mahubani H.M.;
RT "A developmentally regulated cysteine proteinase in Dictyostelium
RT discoideum.";
RL EMBO J. 4:999-1006(1985).
RN [2]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=96210028; PubMed=8631906;
RA Mehta D.P., Ichikawa M., Salimath P.V., Etchison J.R., Haak R.,
RA Manzi A., Freeze H.H.;
RT "A lysosomal cysteine proteinase from Dictyostelium discoideum
RT contains N-acetylglucosamine-1-phosphate bound to serine but not
RT mannose-6-phosphate on N-linked oligosaccharides.";
RL J. Biol. Chem. 271:10897-10903(1996).
CC -!- FUNCTION: CYSTEINE PROTEINASES 1 AND 2 ARE BELIEVED TO PARTICIPATE
CC IN THE BREAKDOWN OF PROTEIN DURING DIFFERENTIATION OF
CC DICTYOSTELIUM AS A RESPONSE TO STARVATION.
CC -!- PTM: PHOSPHOGLYCOSYLATED. CONTAINS GLCNAC-ALPHA-1-P-SER RESIDUES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC -----
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EMBL: X02407; CAA26255.1; --
 DR PIR: A22827; KHDO.
 DR HSSP: P25779; IAIM.
 DR MEROPS: C01.0PA; --
 DR GlycoSuiteDB: P04988; --
 DR SWISS-2DPAGE: P04988; DICTY.
 DR DictyDb: DD02003; cprA.
 DR InterPro: IPR000668; Peptidase_C1.
 DR InterPro: IPR000169; SHprot_acsite.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAPAIN.
 DR PRODOM: P0000158; Peptidase_C1; 1.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
 DR Hydrolase: Thiol protease; Lysosome; Zymogen; Glycoprotein;
 KW Phosphorylation; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 117 ACTIVATION PEPTIDE.
 FT CHAIN 118 343 CYSTEINE PROTEINASE 1.
 FT ACT_SITE 142 142 BY SIMILARITY.
 FT ACT_SITE 286 286 BY SIMILARITY.
 FT ACT_SITE 311 311 BY SIMILARITY.
 FT ACT_SITE 139 190 BY SIMILARITY.
 FT DISULFID 173 224 BY SIMILARITY.
 FT DISULFID 279 332 BY SIMILARITY.
 SQ SEQUENCE 343 AA; 71804C15F2B361E2 CRC64;

Query Match 70.88; Score 34; DB 1; Length 343;
 Best Local Similarity 66.78; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSSYPPT 9
 Db 209 QTSSYPPT 217

RESULT 7
 KVLV_HUMAN
 ID KVLV_HUMAN STANDARD; PRT; 108 AA.
 AC P01604;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Kue.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79237924; PubMed=112021;
 RA Eulitz M., Kley H.-P., Zeitler H.-J.
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid
 sequence of the variable part of a human I-chain of the kappa-type.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 PTR: A01870; KIHUKU.
 DR HSSP: P01607; IREI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 906679A5D90E4E98 CRC64;

Query Match 68.88; Score 33; DB 1; Length 108;
 Best Local Similarity 66.78; Pred. No. 5.2;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSSYPPT 9
 Db 89 QQYSRYPT 97

RESULT 8
 YDE9_SCHPO
 ID YDE9_SCHPO STANDARD; PRT; 345 AA.
 AC Q10442;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Putative mitochondrial carrier C12B10.09.
 GN SPAC12B10.09.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rayndream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,
 RA Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (Potential).
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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CC EMBL; 270721; CAA94699.1; -
DR InterPro; IPR001993; Mitoch_carrter.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KW Transmembrane; Transport.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 83 103 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
FT TRANSMEM 296 316 POTENTIAL.
FT TRANSMEM 319 339 POTENTIAL.
SQ SEQUENCE 345 AA; 38451 MW; 39081A6AAC984B2C CRC64;

Query Match 68.8%; Score 33; DB 1; Length 345;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
   ||| |||
Db 290 QORLSVFT 298

RESULT 9
PPBD_BACSU STANDARD; PRT; 556 AA.
AC P42251;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alkaline phosphatase D precursor (EC 3.1.3.1) (APASED) (RAN1) (BC6).
GN PHOD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 57-76.
RX STRAIN=168 / JH642;
RX MEDLINE=96349109; PubMed=8760916;
RA Eder S., Shi L., Jensen K., Yamane K., Hulett F.M.;
RT "A Bacillus subtilis secreted phosphodiesterase/alkaline phosphatase
is the product of a pho regulon gene, phod.";
RL Microbiology 142:2041-2047(1996).
RN [2]
RP SEQUENCE OF 95-556 FROM N.A.
RX STRAIN=168;
RX MEDLINE=95219079; PubMed=7704254;
RA Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
RT "Determination of a 21548 bp nucleotide sequence around the 24
degrees region of the Bacillus subtilis chromosome.";
RL Microbiology 141:269-275(1995).
RN [3]
RP CHARACTERIZATION.
RX STRAIN=6060-BC6;
RX MEDLINE=78171419; PubMed=25878;
RA Yamane K., Maruo B.;
RT "Purification and characterization of extracellular soluble and
membrane-bound insoluble alkaline phosphatases possessing
phosphodiesterase activities in Bacillus subtilis.";
RL J. Bacteriol. 134:100-107(1978).
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O -> an
alcohol + phosphate
CC -1- INDUCTION: BY PHOSPHATE STARVATION.
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CC EMBL; U49060; AAB47803.1; -
DR EMBL; D30808; BAA06483.1; -
DR EMBL; Z99105; CAB12056.1; -
DR Subtilist; BG11174; phod.
KW Hydrolase; Signal; Complete proteome.
FT SIGNAL 1 56
FT CHAIN 57 556 ALKALINE PHOSPHATASE D.
FT VARIANT 59 59 N -> K.
SQ SEQUENCE 556 AA; 62829 MW; 125F7FDDA08817E3 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSYPFT 9
   |||||
Db 61 SSYPFT 66

RESULT 10
YLN9_CAEEL STANDARD; PRT; 662 AA.
ID YLN9_CAEEL
AC Q09512;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical 76.7 kDa protein D2013.9 in chromosome II.
GN D2013.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Mortimore B., Matthews P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SET DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 TTL DOMAIN.
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CC EMBL; 247808; CAA87778.1; -
DR EMBL; 247809; CAA87778.1; JOINED.
DR EMBL; 247809; CAA87783.1; -
DR EMBL; 247808; CAA87783.1; JOINED.
DR WormPep; D2013.9; CE01535.
DR InterPro; IPR001214; SET.
DR InterPro; IPR004344; Tub_tyr_lygase.
DR Pfam; PF03133; TTL; 1.
DR PROSITE; PS50280; SET; 1.
KW Hypothetical protein.
FT DOMAIN 209 260 SET.
FT DOMAIN 370 662 TTL.
SQ SEQUENCE 662 AA; 76750 MW; 5044C76422145698 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 662;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
   ||| |||
Db 3 EDRAIYFFS 11

RESULT 11
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TF2D_STRPU
ID TF2D_STRPU STANDARD; PRT; 265 AA.
AC P91809;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription initiation factor TFIIID (TATA-box factor)
DE (TATA sequence-binding protein) (TBP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Rybacki D., Childs G.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
CC OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIIID BINDS
CC SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
CC THE POSITION OF TRANSCRIPTION INITIATION.
CC -1- SUBUNIT: BINDS DNA AS A MONOMER.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE TBP FAMILY.
-----
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DR EMBL; U86586; AAB47272.1; -
DR HSSP; P20226; ITGH.
DR InterPro; IPR000814; TFIIID.
DR Pfam; PF00352; TBP; 2.
DR PRINTS; IP00686; TIFACTORIID.
DR PROSITE; PS00351; TFIIID; 2.
KW Transcription regulation; DNA-binding; Nuclear protein; Repeat.
FT REPEAT 91 167
FT REPEAT 181 258
FT REPEAT 181 258
SQ SEQUENCE 265 AA; 29107 MW; 53AED314D2D98926 CRC64;
Query Match 66.7%; Score 32; DB 1; Length 265;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QORSSYP 7
Db 23 QORSHYP 29
RESULT 12
CN7B_MOUSE
ID CN7B_MOUSE STANDARD; PRT; 446 AA.
AC Q9QXQ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
DE PDE7B.
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT "Cloning and characterization of PDE7B, a CAMP-specific
RT phosphodiesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
```

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[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterization of the human and mouse PDE7B, a novel
RT CAMP-specific nucleotide phosphodiesterase."
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -1- PATHWAY: Cyclic nucleotide metabolism.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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DR EMBL; AF190639; AAF25195.1; -
DR EMBL; AJ251859; CAB92530.1; -
DR MGD; MGI-1352752; Pde7b.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR Pfam; PF002073; PDEase.
DR PRINTS; PR00233; PDEase; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP.
FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5A8 CRC64;
Query Match 66.7%; Score 32; DB 1; Length 446;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QORSSYP 8
Db 41 ERGSSYP 48
RESULT 13
CN7B_HUMAN
ID CN7B_HUMAN STANDARD; PRT; 450 AA.
AC Q9NP56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
DE PDE7B.
GN PDE7B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Brain;
RX MEDLINE=20275458; PubMed=10814504;
RA Sasaki T., Kotera J., Yuasa K., Omori K.;
RT "Identification of human PDE7B, a CAMP-specific phosphodiesterase."
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
RL [2]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
FT CAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY DIPHIDAMOLE, IBMX AND SCH51866.
CC -!- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. ALSO EXPRESSED IN
CC HEART, LIVER, SKELETAL MUSCLE AND PANCREAS.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AB038040; BAA96537.1; -.
DR EMBL; AJ251860; CAB92441.1; -.
DR Genbank; HGNC:8792; PDE7B.
DR MIM; 604645; -.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP.
FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 450;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPF 8
Db 41 ERRGSYPF 48
::| |||

RESULT 14
SCD5_YEAST
ID SCD5_YEAST STANDARD; PRT; 872 AA.
AC P34758;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SCD5 protein (FTB1 protein).
GN SCD5 OR FTB1 OR YOR329C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX PubMed=8688556;
RA Nelson K.K., Holmer M., Lemmon S.K.;
RT "SCD5, a suppressor of clathrin deficiency, encodes a novel protein
RT with a late secretory function in yeast.";
```

```
RL Mol. Biol. Cell 7:245-260(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Wang W., Zheng L., Chan C.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RA Song J.M., Cheung E., Rabinowitz J.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051586; PubMed=8896263;
RA Parle-Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
RT "Sequence of 29 kb around the PDR10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I.";
RL Yeast 12:999-1004(1996).
CC -!- FUNCTION: Involved in vesicular transport at a late stage of the
CC secretory pathway.
CC -!- SUBUNIT: PUTATIVE 10-FORMYL-TETRAHYDROFOLATE BINDING PROTEIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -----
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CC -----
DR EMBL; U03492; AAR09719.1; -.
DR EMBL; U42227; AAR85443.1; -.
DR EMBL; Z49821; CAA89976.1; -.
DR EMBL; Z75237; CAA99650.1; -.
DR SGD; S0005856; SCD5.
KW Transport; Protein transport; Membrane; Repeat.
FT DOMAIN 405 448 3 X 20 AA APPROXIMATE REPEATS.
FT REPEAT 405 424 1-1.
FT REPEAT 439 458 1-2.
FT REPEAT 479 498 1-3.
FT DOMAIN 534 728 9 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 534 545 2-1.
FT REPEAT 564 575 2-2.
FT REPEAT 593 604 2-3.
FT REPEAT 608 619 2-4.
FT REPEAT 623 634 2-5.
FT REPEAT 636 647 2-5.
FT REPEAT 650 661 2-7.
FT REPEAT 683 694 2-8.
FT REPEAT 717 728 2-9.
SQ SEQUENCE 872 AA; 97305 MW; C60F5BE8808EID31 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 872;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPF 9
Db 831 QOQQQFPF 839
::| |||

RESULT 15
AT7A_CRIGR
ID AT7A_CRIGR STANDARD; PRT; 1476 AA.
AC P49015;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Copper-transporting ATPase 1 (EC 3.6.3.4) (Copper pump 1)
DE (Fragment).
GN ATP7A.
```

OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_Taxid-10029;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-K16
RX MEDLINE-960154683; PubMed-8589689;
RA Canakaris J., Petris M.J., Bailey L., Shen P., Lockhart P.,
RA Glover T.W., Barcroft C., Patton J., Mercer J.F.;
RT "Gene amplification of the Menkes (MNK; ATP7A) P-type ATPase gene of
RT CHO cells is associated with copper resistance and enhanced copper
RT efflux."
RL Hum. Mol. Genet. 4:2117-2123(1995).
CC -1- FUNCTION: MAY FUNCTION IN THE EXPORT OF COPPER FROM THE CYTOPLASM
CC TO AN INTRACELLULAR ORGANELLE. IT MAY SERVE AS WELL FOR THE EXPORT
CC OF OTHER METALS.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+)(In) = ADP + phosphate +
CC Cu(2+)(Out).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN MOST TISSUES EXCEPT LIVER.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES).
CC -1- SIMILARITY: CONTAINS 6 HMA DOMAINS.
CC
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CC -----
CC EMBL; U23946; AAB39918.1; -.
CC HSPP; Q04656; IAWO.
DR InterPro: IPR001757; ATPase_E1-E2.
DR InterPro: IPR001934; HeavyMe_transpt.
DR InterPro: IPR001454; Hignase/hydrilase.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00403; HMA; 6.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR00003; HMA; 6.
DR PROSITE; PS00154; ATPase_E1_E2; 1.
DR PROSITE; PS01047; HMA_1; 5.
DR PROSITE; PS00846; HMA_2; 6.
KW Hydrolyase; Copper transport;
KW ATP-binding; Metal-binding; Transmembrane; Phosphorylation;
KW ATP-binding; Metal-binding; Copper; Repeat.
FT DOMAIN 1 642
FT TRANSMEM 643 665 POTENTIAL.
FT TRANSMEM 695 717 POTENTIAL.
FT TRANSMEM 736 760 POTENTIAL.
FT TRANSMEM 770 788 POTENTIAL.
FT TRANSMEM 930 952 POTENTIAL.
FT TRANSMEM 978 998 POTENTIAL.
FT TRANSMEM 1347 1373 POTENTIAL.
FT TRANSMEM 1379 1397 POTENTIAL.
FT DOMAIN 9 75
FT DOMAIN 172 238 HMA 2.
FT DOMAIN 277 343 HMA 3.
FT DOMAIN 377 443 HMA 4.
FT DOMAIN 479 545 HMA 5.
FT DOMAIN 555 621 HMA 6.
FT MOD_RES 1034 1034 PHOSPHORYLATION (PROBABLE).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 685 685 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 887 887 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 953 953 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1130 1130 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1134 1134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 1476 1476 N-LINKED (GLCNAC. .) (POTENTIAL).
FT

SQ SEQUENCE 1476 AA; 160335 MW; 6B36F5A2AC358C0B CRC64;
Query Match 66.7%; Score 32; DB 1; Length 1476;
Best Local Similarity 85.7%; Pred. NO. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QORSSYP 7
Db 267 QORPSYP 273
Search completed: December 23, 2002, 07:26:10
Job time : 2.88953 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 3.73256 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	79.2	134	11 Q8VDD0	Q8vdd0 mus musculus
2	37	77.1	106	5 Q9U410	Q9u410 schistosoma
3	37	77.1	269	5 Q18582	Q18582 caenorhabdi
4	37	77.1	289	13 Q8U0Z5	Q8uuz5 brachydanio
5	36	75.0	886	16 Q9KC72	Q9kc72 bacillus ha
6	35	72.9	108	11 Q8VIJ0	Q8vij0 mus musculus
7	35	72.9	133	3 Q12744	Q12744 saccharomyc
8	34	70.8	341	16 Q8X6Y8	Q8x6y8 escherichia
9	34	70.8	363	10 Q9SWC7	Q9swc7 glycine max
10	34	70.8	377	10 Q24324	Q24324 phaseolus v
11	34	70.8	380	10 Q43448	Q43448 glycine max
12	34	70.8	393	5 Q96635	Q96635 trypanosoma
13	34	70.8	397	16 Q35007	Q35007 bacillus su
14	34	70.8	399	16 Q9K6Q6	Q9k6q6 bacillus ha
15	34	70.8	478	5 Q96750	Q96750 trypanosoma
16	34	70.8	653	3 Q12171	Q12171 saccharomyc

17	34	70.8	721	16 Q99YL1	Q99yl1 streptococc
18	34	70.8	977	5 Q97357	Q97357 trypanosoma
19	34	70.8	1138	16 Q92KB6	Q92kb6 rhizobium m
20	34	70.8	1194	5 Q9VSI2	Q9vsi2 drosophila
21	33	68.8	169	5 Q8SVY7	Q8svy7 encephalito
22	33	68.8	234	11 Q8R062	Q8r062 mus musculu
23	33	68.8	246	13 Q9W6E5	Q9w6e5 gallus gall
24	33	68.8	380	3 Q9P8H2	Q9p8h2 cryptococcu
25	33	68.8	434	5 Q94503	Q94503 dictyosteli
26	33	68.8	539	5 Q9V490	Q9v490 drosophila
27	33	68.8	543	5 Q961N4	Q961n4 drosophila
28	33	68.8	543	5 Q9XZC2	Q9xzc2 drosophila
29	33	68.8	580	10 Q9SIV8	Q9siv8 arabidopsis
30	33	68.8	685	16 Q92TJ0	Q92tj0 rhizobium m
31	33	68.8	733	13 Q91817	Q91817 xenopus lae
32	33	68.8	1108	5 Q8T2E2	Q8t2e2 dictyosteli
33	33	68.8	3232	3 Q94205	Q94205 clavicaps p
34	32	66.7	196	5 Q9VDZ9	Q9vdz9 drosophila
35	32	66.7	210	5 Q95SL8	Q95sl8 drosophila
36	32	66.7	210	5 Q9W3R3	Q9w3r3 drosophila
37	32	66.7	237	5 Q8SXD8	Q8sxd8 drosophila
38	32	66.7	250	17 Q8TIX4	Q8tix4 methanosarc
39	32	66.7	271	5 Q77208	Q77208 lytechninus
40	32	66.7	374	2 Q69413	Q69413 escherichia
41	32	66.7	374	16 Q85626	Q85626 escherichia
42	32	66.7	412	12 Q8QRX0	Q8qrx0 chimpanzee
43	32	66.7	422	4 Q8BZ40	Q8bz40 homo sapien
44	32	66.7	428	5 Q8SXA2	Q8sxa2 drosophila
45	32	66.7	446	11 Q8VIE4	Q8vie4 rattus norv

ALIGNMENTS

RESULT 1

Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Sembi P.;
RT "Targeting T cells to the CNS";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CDFD8E2236E2D0CF CRC64;

Query Match 79.2%; Score 38; DB 11; Length 134;
Best Local Similarity 87.5%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9

```
|||||:|
Db 111 QRSSPWT 118

RESULT 2
Q9U410 ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RN SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."; to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
FT SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 77.1%; Score 37; DB 5; Length 106;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRSSYPPT 9
||:|||||
Db 88 QQWTSYPPT 96

RESULT 3
Q18582 ID Q18582 PRELIMINARY; PRT; 269 AA.
AC Q18582;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 30.8 kDa protein.
GN C42D8.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RN [2]
RN "Genome sequence of the nematode C. elegans: a platform for
RN investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [3]
RN SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Hallsworth K.;
RT "The sequence of C. elegans cosmid C42D8.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC Bacteria; Firmicutes; Bacillus/clostridium group; Bacillales;

Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U56966; AAA98721.2; -.
KW Hypothetical protein.
SQ SEQUENCE 269 AA; 30847 MW; 32D2B7A1C0102F93 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 269;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRSSYPPT 9
||:|||||
Db 225 QRRENYPPT 233

RESULT 4
Q8U0Z5 ID Q8U0Z5 PRELIMINARY; PRT; 289 AA.
AC Q8U0Z5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Orthodenticle-related homeobox 5.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RN SEQUENCE FROM N.A.
RA Gamse J.T., Liang J.O., Shen Y.-C., Raymond P., Thisse B., Thisse C.,
RA Halpern M.E.;
RT "Otx5 regulates genes that show circadian expression in the zebrafish
RT pineal complex.";
RL Nat. Genet. 30:117-121(2002).
DR EMBL; AY036005; AAK62029.1; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_repressr.
DR InterPro; IPR003025; Otx_TF.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF03529; TF_Otx; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRINTS; PR01255; OTXHOMEBOX.
DR PRODom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 289 AA; 31422 MW; 542FA0F69AE90DAC CRC64;

Query Match 77.1%; Score 37; DB 13; Length 289;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSSYPPT 9
|||||:|
Db 177 QRSSYPPT 184

RESULT 5
Q9KC72 ID Q9KC72 PRELIMINARY; PRT; 886 AA.
AC Q9KC72;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Penicillin-binding proteins 1A/1B.
GN PONA OR BH1702.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/clostridium group; Bacillales;
```

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OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05421.1; -.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR001264; GT.51.
DR InterPro; IPR001460; Transpeptidase.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00912; transglycosyl; 1.
DR Pfam; PF00903; Transpeptidase; 1.
DR ProDom; PD001895; GT.51; 1.
DR SMART; SM00060; FN3; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 886 AA; 98280 MW; 0562807F75148534 CRC64;

Query Match 75.0%; Score 36; DB 16; Length 886;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPF 8
Db 282 QERESYPF 289
[1] [1] [1] [1]

RESULT 6
Q8VIJ0 PRELIMINARY; PRT; 108 AA.
ID Q8VIJ0;
AC Q8VIJ0;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VK19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ-LPR/LPR;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis."
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 72.9%; Score 35; DB 11; Length 108;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPF 9
Db 89 QQYNSYPF 97
[1] [1] [1] [1]

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RESULT 7
Q12744 PRELIMINARY; PRT; 133 AA.
ID Q12744;
AC Q12744;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical ORF IDENTICAL to ORF NOTED in RAD10 5' region A22726.
GN YML095C-A.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Gentles S., Bowman S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBDJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Barrell B., Rajandream M.A.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP SEQUENCE OF 2-133 FROM N.A.
RX MEDLINE=85284950; PubMed=3896774;
RA Weiss W.A., Friedberg E.C.;
RT "Molecular cloning and characterization of the yeast RAD10 gene and
RT expression of RAD10 protein in E. coli."
RL EMBO J. 4:1575-1582(1985).
DR EMBL; Z46660; CAA86643.1; -.
DR EMBL; X02591; CAA26432.1; -.
DR SGB; S0004561; YML095C-A.
DR InterPro; IPR002016; Peroxidase.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
SQ SEQUENCE 133 AA; 15007 MW; B93007588867456 CRC64;

Query Match 72.9%; Score 35; DB 3; Length 133;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPF 9
Db 101 QORRSYSFT 109
[1] [1] [1] [1]

RESULT 8
Q8X6Y8 PRELIMINARY; PRT; 341 AA.
ID Q8X6Y8;
AC Q8X6Y8;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Putative capsid protein of prophage Cp-933X (Putative major capsid
DE protein).
GN Z1888 OR ECS2174 OR ECS1635.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouisis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RT Nature 409:529-533(2001).

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[2]
RN SEQUENCE FROM N.A.
RP STRAIN=0157:H7 / RIMD 0509952;
RX MEDLINE=21556231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RL DNA Res. 8:11-22(2001).";
DR EMBL; AB005330; AAG55985.1; -.
DR EMBL; AP002557; BAB35597.1; -.
DR EMBL; AB002555; BAB35058.1; -.
KW Complete proteome.
SQ SEQUENCE 341 AA; 38123 MW; C0310C4DE97C0037 CRC64;

Query Match 70.8%; Score 34; DB 16; Length 341;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSVPPT 9
Db 29 RESVPPT 35

RESULT 9
Q9SWC7 PRELIMINARY; PRT; 363 AA.
ID Q9SWC7
AC Q9SWC7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative cysteine proteinase GmpM33.
GN GMPM33.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SHI-SHI;
RA Chow T.-Y., Liu S.-M., Lin T.-X., Hsing Y.-I.C.;
RT "Characterization of soybean seed maturation protein, PM33.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0467986; AAD46920.1; -.
DR HSSP; P25779; IAIM.
DR InterPro; IPR000668; Peptidase_C1.
DR Pfam; PF00112; Peptidase_C1.
DR PRINTS; PR00705; PAPAIN.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolase; Thiol protease.
SQ SEQUENCE 363 AA; 39685 MW; 55C46B8F2CACB8FB CRC64;

Query Match 70.8%; Score 34; DB 10; Length 363;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSVPPT 9
Db 213 EEESVPPT 221

RESULT 10
O24324 PRELIMINARY; PRT; 377 AA.
ID O24324
AC O24324;
DT 01-JAN-1998 (TREMBlrel. 05, Created)

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DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cysteine proteinase precursor.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MOLDAVIAN; TISSUE=COTYLEDON;
RA Senyuk V., Becker C., Muentz K.;
RT "Isolation of cDNA clone encoding cysteine proteinase (CP4) from a
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99955; CAB17077.1; -.
DR HSSP; P25779; IAIM.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_actsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
KW Hydrolase; Signal; Thiol protease.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 138 377 CYSTEINE PROTEINASE.
SQ SEQUENCE 377 AA; 41827 MW; 6576DEF3F1B26DA9 CRC64;

Query Match 70.8%; Score 34; DB 10; Length 377;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSVPPT 9
Db 228 EEESVPPT 236

RESULT 11
Q43448 PRELIMINARY; PRT; 380 AA.
ID Q43448
AC Q43448;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cysteine proteinase precursor.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FISKEY V; TISSUE=COTYLEDON;
RX MEDLINE=95260869; PubMed=7742372;
RA Nong V., Becker C., Muentz K.;
RT "cDNA cloning for a putative cysteine proteinase from developing seeds
of soybean.";
RL Biochim. Biophys. Acta 1261:435-438(1995).
DR EMBL; Z32795; CAA83673.1; -.
DR HSSP; P25779; IAIM.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_actsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolase; Signal; Thiol protease.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 140 380 CYSTEINE ENDOPEPTIDASE.
SQ SEQUENCE 380 AA; 41590 MW; 902A93F8132D56C1 CRC64;

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Query Match 70.8%; Score 34; DB 10; Length 380;
 Best Local Similarity 55.6%; Pred. No. 61;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRSSYPT 9
 DB 230 EESSYPT 238
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RESULT 12
 O96635 PRELIMINARY; PRT; 393 AA.
 AC O96635;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Lysosomal alpha mannosidase (fragment).
 OS O20.
 GN Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL BRENER;
 RX MEDLINE=20160916; PubMed=1068909;
 RA Vazquez M.P., Ben-Dov C.P., Lorenzi H.A., Moore T., Schijman A.G.,
 RA Levin M.J.;
 RT "The short interspersed repetitive element of Trypanosoma cruzi, SIRE,
 is associated to VIPER, a novel and unusual retroelement related to
 LTR-retrotransposons.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:2128-2133(2000).
 DR EMBL: AF096926; AAC72969.1;
 FT NON_TER 1
 SQ SEQUENCE 393 AA; 44188 MW; A728125DDA5CA282 CRC64;

Query Match 70.8%; Score 34; DB 5; Length 393;
 Best Local Similarity 85.7%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPT 9
 DB 147 RSDYPT 153
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RESULT 13
 O35007 PRELIMINARY; PRT; 397 AA.
 AC O35007;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE YVRP protein.
 GN YVRP.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borris R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Gutseppl G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Rochet B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RL Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Wipat A., Brignell C.S., Guy J.B., Rose M., Emerson P.T.,
 RA Harwood C.R.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 4-397 FROM N.A.
 RC STRAIN=168;
 RA Rose M., Entian K.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Harwood C.R.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99120; CAB15319.1;
 DR EMBL; Z99121; CAB15334.1;
 DR EMBL; AJ223978; CAA11723.1;
 KW Complete proteome.
 SQ SEQUENCE 397 AA; 43492 MW; 9FBF8280458AD7CF CRC64;

Query Match 70.8%; Score 34; DB 16; Length 397;
 Best Local Similarity 75.0%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPT 9
 DB 288 QSSNYPT 295
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RESULT 14
 Q9K606 PRELIMINARY; PRT; 399 AA.
 ID Q9K606
 AC Q9K606;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE ABC transporter.
 GN BH3672.
 OS Bacillus halodurans.
 GN Bacillus; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacteria; Firmicutes; Bacillus.
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RL halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001519; BAB07391.1; -;
 KW Complete proteome.
 SQ SEQUENCE 399 AA; 45051 MW; 4FASD772A8D3960C CRC64;

Query Match 70.8%; Score 34; DB 16; Length 399;
 Best Local Similarity 75.0%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
 Db 287 QSSNYPFT 294

RESULT 15
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 AC O96750;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ESAG5 protein.
 DE ESAG5.
 GN Trypanosoma brucei rhodesiense.
 OS Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=31286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EA7RO 3;
 RX MEDLINE=99081299; PubMed=9865701;
 RA Xong H.V., Vanhamme L., Chamekh M., Chimfwembe E.C.,
 RA Van den Abbeele J., Pays A., van Meirvenne N., Hamers R.,
 RA de Batselier P., Pays E.;
 RT "A VSG expression site-associated gene confers resistance to human
 RL serum in Trypanosoma rhodesiense.";
 RL Cell 95:839-846(1998).
 DR EMBL; AJ010094; CAA09000.1; -;
 SQ SEQUENCE 478 AA; 52703 MW; 3CC5004781E5B97F CRC64;

Query Match 70.8%; Score 34; DB 5; Length 478;
 Best Local Similarity 87.5%; Pred. No. 77;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
 Db 28 QRSSSPT 35

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 Job time : 5.73256 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 21.0872 seconds
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163.250 Million cell updates/sec

Title: US-09-865-198-7
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
1	554.5	87.9	535	4	US-08-983-035A-38
2	532.5	84.4	118	3	US-08-767-128-22
3	513.5	81.4	270	2	US-08-652-507-2
4	507.5	80.4	124	1	US-08-017-570-6
5	507.5	80.4	124	1	US-08-471-426-6
6	507.5	80.4	124	5	PCT-US94-01709-6
7	507.5	80.4	553	2	US-08-661-052-16
8	507.5	80.4	553	4	US-09-188-082-16
9	507.5	80.4	553	4	US-09-364-088-16
10	507.5	80.4	553	4	US-09-102-716-16
11	502.5	79.6	124	1	US-08-017-570-4
12	502.5	79.6	124	1	US-08-471-426-4
13	502.5	79.6	124	5	PCT-US94-01709-4
14	499.5	79.2	124	4	US-09-672-609-1
15	499.5	79.2	124	4	US-09-025-403A-1
16	498.5	79.0	281	4	US-09-423-439-44
17	498.5	79.0	642	4	US-09-423-439-26
18	498.5	79.0	666	4	US-09-423-439-51
19	495.5	78.5	255	4	US-09-171-945-19
20	481.5	76.3	136	4	US-08-348-548-8
21	481.5	76.3	136	5	PCT-US95-15716-8
22	480.5	76.1	120	4	US-09-171-945-11
23	480	76.1	125	2	US-08-561-521-44
24	480	76.1	125	5	PCT-US95-01219-44
25	478	75.8	117	2	US-08-290-592E-18
26	478	75.8	117	5	PCT-US95-10053-15
27	478	75.8	117	5	PCT-US96-09448-18

28	475	75.3	136	4	US-08-646-265A-29	Sequence 29, Appl
29	470.5	74.6	118	2	US-08-232-081B-38	Sequence 38, Appl
30	468	74.2	123	2	US-08-561-521-9	Sequence 9, Appl
31	468	74.2	123	5	PCT-US95-01219-9	Sequence 9, Appl
32	466	73.9	121	2	US-08-822-830B-13	Sequence 13, Appl
33	463	73.4	121	2	US-08-822-830B-2	Sequence 2, Appl
34	461	73.1	120	2	US-08-950-660-2	Sequence 2, Appl
35	461	73.1	120	5	PCT-US93-00030-2	Sequence 2, Appl
36	461	73.1	120	5	PCT-US93-00924-2	Sequence 2, Appl
37	460	72.9	140	2	US-08-561-521-4	Sequence 4, Appl
38	460	72.9	140	5	PCT-US95-01219-4	Sequence 4, Appl
39	458	72.6	136	1	US-08-024-253-2	Sequence 4, Appl
40	452	71.6	254	2	US-08-792-824-4	Sequence 4, Appl
41	452	71.6	254	2	US-08-792-824-7	Sequence 7, Appl
42	452	71.6	254	2	US-08-792-824-10	Sequence 10, Appl
43	452	71.6	254	2	US-08-792-824-13	Sequence 13, Appl
44	450.5	71.4	120	4	US-08-871-488A-15	Sequence 15, Appl
45	447.5	70.9	113	1	US-08-207-169A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-983-035A-38
; Sequence 38, Application US/08983035A
; Patent No. 6326464
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,035A
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01111
; FILING DATE: 17-JUL-1996
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Strauss, William L.
; REGISTRATION NUMBER: 47,114
; REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

Query Match 87.9%; Score 554.5; DB 4; Length 535;
Best Local Similarity 88.9%; Pred. No. 5.1e-48;

Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Qy 1 QVKLQSGAELVGSASVKLSCTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
Db 3 QVQLQSGAELVGSASVKLSCTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDTTEY 62
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTVTTVSS 117
Db 63 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTVTTVSS 118

RESULT 2

US-08-767-128-22
; Sequence 22, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

US-08-767-128-22

Query Match 84.4%; Score 532.5; DB 3; Length 118;
Best Local Similarity 85.6%; Pred. No. 1.4e-46;
Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVKLQSGAELVGSASVKLSCTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
Db 1 EVQLQSGAELVRSASVKLSCTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDTTEY 60
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTVTTVSS 117
Db 61 DPKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTVTTVSS 118

RESULT 3

US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691

GENERAL INFORMATION:

APPLICANT:
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Giebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/08/652,507
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-652-507-2

Query Match 81.4%; Score 513.5; DB 2; Length 270;
Best Local Similarity 81.3%; Pred. No. 3e-44;
Matches 100; Conservative 4; Mismatches 10; Indels 9; Gaps 2;

Qy 1 QVKLQSGAELVGSASVKLSCTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
Db 27 QVQLQSGAELVRSCTSGFNKIDSYMHVWKQRPQGLEWIGWIDPENGDTTEY 86
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTVTTVT 114
Db 87 APKFGKATMTDSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTVTTVT 143
Qy 115 VSS 117
Db 144 VSS 146

RESULT 4

US-08-017-570-6
; Sequence 6, Application US/08017570

Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOW, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-6

Query Match 80.4%; Score 507.5; DB 1; Length 124;
Best Local Similarity 77.2%; Pred. No. 4.8e-44;
Matches 98; Conservative 8; Mismatches 8; Indels 13; Gaps 2;

QY 1 OVKLOQSGAELVSGASVKLSCTTSGFNKDYMHVWVQRPEQGLEWIGWIDPENGDSGY 60
Db 1 EVOLQSGAELVRSASVKMSCTASGFNKKDYMHVWVQRPEQGLEWIGWIDPENGDTY 60

QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YYGDYEGYWGOG 110
Db 61 APKFGKATMTDTSNTAYLQLSLTSEDYAVYYCNRGLSTMTITRWFDD---VWGAG 117

QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 5
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOW, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967

; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match 80.4%; Score 507.5; DB 1; Length 124;
Best Local Similarity 77.2%; Pred. No. 4.8e-44;
Matches 98; Conservative 8; Mismatches 8; Indels 13; Gaps 2;

QY 1 OVKLOQSGAELVSGASVKLSCTTSGFNKDYMHVWVQRPEQGLEWIGWIDPENGDSGY 60
Db 1 EVOLQSGAELVRSASVKMSCTASGFNKKDYMHVWVQRPEQGLEWIGWIDPENGDTY 60

QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YYGDYEGYWGOG 110
Db 61 APKFGKATMTDTSNTAYLQLSLTSEDYAVYYCNRGLSTMTITRWFDD---VWGAG 117

QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 6
PCT-US94-01709-6
; Sequence 6, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

; NAME: OLMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01709-6

Query Match      80.4%; Score 507.5; DB 5; Length 124;
Best Local Similarity 77.2%; Pred. No. 4.8e-44;
Matches 98; Conservative 8; Mismatches 8; Indels 13; Gaps 2;

QY 1 QVKKQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
DB 1 EVQKQSGAELVSGASVKLSCTAGFNKDYMHVWKORPEQGLEWIGWIDPENGDTGY 60
QY 61 APKQGGKATMTADSSNTAYLQLSLTSEDYAVYCN-----YYGDYEGYWGQTTVV 110
DB 61 APKQGGKATMTDSSNTAYLQLSLTSEDYAVYCNTRGLSTMTTTRWFFD---VWGAG 117
QY 111 TTVTVSS 117
DB 118 TTVTVSS 124

RESULT 7
US-08-661-052-16
; Sequence 16; Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-5941
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match      80.4%; Score 507.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 2.8e-43;
Matches 98; Conservative 5; Mismatches 10; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGYA 61
DB 278 IKLQSGAELVRSCTSVKLSCTAGFNKDSYMHVLRQGPQGLEWIGWIDPENGDTGYA 337
QY 62 PKFGKATMTADSSNTAYLQLSLTSEDYAVYCN-----YYGDYEGYWGQTTVV 115
DB 338 PKFGKATMTDSSNTAYLQLSLTSEDYAVYCNTRGLSTMTTTRWFFD---YWGQTTVV 394
QY 116 SS 117
DB 395 SS 396

RESULT 8
US-09-188-082-16
; Sequence 16; Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-188-082-16

Query Match      80.4%; Score 507.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 2.8e-43;
Matches 98; Conservative 5; Mismatches 10; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGYA 61
DB 278 IKLQSGAELVRSCTSVKLSCTAGFNKDSYMHVLRQGPQGLEWIGWIDPENGDTGYA 337
QY 62 PKFGKATMTADSSNTAYLQLSLTSEDYAVYCN-----YYGDYEGYWGQTTVV 115
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Db 338 PKFOGKATTTDSSNTAYLQLSLTSEDVAVYCNEGTPTGPFYFD---YWGQGTTVTV 394
QY 116 SS 117
Db 395 SS 396

RESULT 9
US-09-364-088-16
; Sequence 16, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-16

Query Match 80.4%; Score 507.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 2.8e-43;
Matches 98; Conservative 5; Mismatches 10; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSFNKIDFYMHVYKQRPQGLEWIGWIDPENGDSGYA 61
Db 278 IKLQSGAELVSRGTSVKLSCTASGNKIDSYMHVLRQGPQGLEWIGWIDPENGDEYA 337

QY 62 PKFOGKATWTADSSNTAYLQLSLTSEDVAVYCN-----AYYGDYEGYWGQGTTVTV 115
Db 338 PKFOGKATTTDSSNTAYLQLSLTSEDVAVYCNEGTPTGPFYFD---YWGQGTTVTV 394

QY 116 SS 117
Db 395 SS 396

RESULT 10
US-09-102-716-16
; Sequence 16, Application US/09102716
```

```
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 80.4%; Score 507.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 2.8e-43;
Matches 98; Conservative 5; Mismatches 10; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSFNKIDFYMHVYKQRPQGLEWIGWIDPENGDSGYA 61
Db 278 IKLQSGAELVSRGTSVKLSCTASGNKIDSYMHVLRQGPQGLEWIGWIDPENGDEYA 337

QY 62 PKFOGKATWTADSSNTAYLQLSLTSEDVAVYCN-----AYYGDYEGYWGQGTTVTV 115
Db 338 PKFOGKATTTDSSNTAYLQLSLTSEDVAVYCNEGTPTGPFYFD---YWGQGTTVTV 394

QY 116 SS 117
Db 395 SS 396

RESULT 11
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOW, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Duane C. Ulmer
;; STREET: P.O. Box 1967
;; CITY: Midland
;; STATE: MI
;; COUNTRY: US
;; ZIP: 48641-1967
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION NUMBER: US/08/017,570
;; FILING DATE: 19930216
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ULMER, DUANE C
;; REGISTRATION NUMBER: 34,941
;; REFERENCE/DOCKET NUMBER: C-38,777
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (517) 636-8104
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-017-570-4
Query Match 79.6%; Score 502.5; DB 1; Length 124;
Best Local Similarity 76.4%; Pred. No. 1.5e-43;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVYKQRPQGLEWIGWIDPENGDSGY 60
Db 1 EVLQSGAELVRSASVKMSCTASGTFNIDYMHVYKQRPQGLEWIGWIDPENGDTGY 60
QY 61 APFQKATMTADSSNTAYLQLSLTSEDVAVYCN-----YGDYEGYWGQ 110
Db 61 APFQKATMTDTSNTAYLQLSLTSEDVAVYCNTRLTMTITRWFFD---VWGAG 117
QY 111 TTVVSS 117
Db 118 TTVAVSS 124
RESULT 12
US-08-471-426-4
; Sequence 4; Application US/08471426
; Patent No. 4580033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/471,426
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/017,570
;; FILING DATE: 16-FEB-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ULMER, DUANE C
;; REGISTRATION NUMBER: 34,941
;; REFERENCE/DOCKET NUMBER: C-38,777
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (517) 636-8104
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-471-426-4
Query Match 79.6%; Score 502.5; DB 1; Length 124;
Best Local Similarity 76.4%; Pred. No. 1.5e-43;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVYKQRPQGLEWIGWIDPENGDSGY 60
Db 1 EVLQSGAELVRSASVKMSCTASGTFNIDYMHVYKQRPQGLEWIGWIDPENGDTGY 60
QY 61 APFQKATMTADSSNTAYLQLSLTSEDVAVYCN-----YGDYEGYWGQ 110
Db 61 APFQKATMTDTSNTAYLQLSLTSEDVAVYCNTRLTMTITRWFFD---VWGAG 117
QY 111 TTVVSS 117
Db 118 TTVAVSS 124
RESULT 13
PCT-US94-01709-4
; Sequence 4; Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

RESULT 15
US-09-025-403A-1
; Sequence 1, Application US/09025403A
; Patent No. 6417337
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.

Search completed: December 23, 2002, 07:33:17
Job time : 23.0872 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 10.8837 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-7

Perfect score: 631

Sequence: 1 QVKLQSGAELVGSASVKL.....AYYGDYEGWGQGTTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_PEP.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB_PEP.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB_PEP.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_PEP.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_PEP.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB_PEP.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	117	10	US-09-976-787-7
2	631	100.0	117	10	US-09-865-198-7
3	631	100.0	240	10	US-09-976-787-28
4	631	100.0	240	10	US-09-865-198-27
5	624	98.9	117	10	US-09-976-787-23
6	624	98.9	117	10	US-09-865-198-22
7	624	98.9	238	10	US-09-976-787-29
8	624	98.9	238	10	US-09-865-198-28
9	499.5	79.2	124	9	US-09-974-051-1
10	499.5	79.2	124	9	US-09-974-051-1
11	498.5	79.0	120	10	US-09-910-059-11
12	498.5	79.0	255	10	US-09-910-059-19
13	484.5	76.8	136	10	US-09-564-329A-11
14	484.5	76.8	136	10	US-09-855-153-11
15	484.5	76.8	136	10	US-09-854-811-11
16	484.5	76.8	136	10	US-09-934-773-11
17	484.5	76.8	136	10	US-09-963-620-11
18	478	75.8	117	10	US-09-158-120A-18
19	428	67.8	117	10	US-09-158-120A-17

20	427.5	67.7	139	10	US-09-809-739-5	Sequence 5, Appli
21	421.5	66.8	244	10	US-09-940-391-1	Sequence 1, Appli
22	413.5	65.5	124	9	US-09-974-052-9	Sequence 9, Appli
23	413.5	65.5	124	9	US-09-974-052-12	Sequence 12, Appli
24	413.5	65.5	124	9	US-09-974-051-9	Sequence 9, Appli
25	413.5	65.5	124	9	US-09-974-051-12	Sequence 12, Appli
26	409.5	64.9	124	9	US-09-974-052-8	Sequence 8, Appli
27	409.5	64.9	124	9	US-09-974-051-8	Sequence 8, Appli
28	406.5	64.7	120	10	US-09-910-059-89	Sequence 89, Appli
29	406.5	64.7	120	10	US-09-998-831-7	Sequence 7, Appli
30	404.5	64.1	120	10	US-09-910-059-79	Sequence 79, Appli
31	402.5	63.8	120	10	US-09-910-059-91	Sequence 91, Appli
32	399.5	63.3	120	10	US-09-910-059-85	Sequence 85, Appli
33	399.5	63.3	122	1	US-08-779-784-28	Sequence 28, Appli
34	399.5	63.3	153	10	US-09-861-294-4	Sequence 4, Appli
35	398.5	63.2	120	10	US-09-910-059-81	Sequence 81, Appli
36	397.5	63.0	120	12	US-10-025-687-2	Sequence 2, Appli
37	397.5	63.0	124	9	US-09-974-052-7	Sequence 7, Appli
38	397.5	63.0	124	9	US-09-974-051-7	Sequence 7, Appli
39	397	62.9	138	10	US-09-753-436-78	Sequence 78, Appli
40	395.5	62.7	120	10	US-09-910-059-55	Sequence 55, Appli
41	395.5	62.7	255	10	US-09-910-059-57	Sequence 57, Appli
42	395.5	62.7	260	10	US-09-910-059-93	Sequence 93, Appli
43	395.5	62.7	306	10	US-09-910-059-95	Sequence 95, Appli
44	395.5	62.7	613	10	US-09-910-059-113	Sequence 113, App
45	395.5	62.7	716	10	US-09-910-059-125	Sequence 125, App

ALIGNMENTS

RESULT 1

US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match	100.0%	Score 631;	DB 10;	Length 117;
Best Local Similarity	100.0%	Pred. No. 6e-42;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKPQPGLEWIGWIDPENGDSGY	60	
Db	1	QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKPQPGLEWIGWIDPENGDSGY	60	
Qy	61	APKFGKATMTADSSNTAYLQLSLTSDTAVYCYNAVYGYEGYWGOGTTVTSS	117	
Db	61	APKFGKATMTADSSNTAYLQLSLTSDTAVYCYNAVYGYEGYWGOGTTVTSS	117	

RESULT 2

US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping

; SOFTWARE: WordPerfect 8.0 for Windows

US-09-910-059-19

1

Search completed: December 23, 2002, 07:58:19
Job time : 10.8837 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 23.1279 seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-7

Perfect score: 631

Sequence: 1 QVKLQSGAELVSGASVKL.....AYYGDYEGYWGQGTITVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	509	80.7	136	2 S04576	Ig heavy chain pre
2	497.5	78.8	268	2 A56446	Ig heavy chain v r
3	494.5	78.4	116	2 S15672	Ig heavy chain v r
4	487	77.2	118	2 S25174	Ig heavy chain v r
5	481.5	76.3	137	2 S52445	Ig heavy chain v r
6	479	75.9	117	2 S17586	Ig heavy chain v r
7	478	75.8	221	2 S49220	Ig gamma-1 chain -
8	475	75.3	120	2 S03471	Ig heavy chain v-D
9	469.5	74.4	178	2 S29594	Ig gamma chain (WM
10	466	73.9	116	2 S24289	Ig gamma chain v r
11	464.5	73.6	114	4 A47271	nitrophenyl phosph
12	460.5	73.0	122	2 S06823	Ig heavy chain v r
13	454	71.9	120	2 S03484	Ig heavy chain v-D
14	453	71.8	115	2 S03482	Ig heavy chain v-D
15	452	71.6	233	2 JC5322	p53 specific singl
16	434	68.8	108	2 PH1012	Ig heavy chain: v r
17	432	68.5	249	2 S41374	single chain Fv an
18	429.5	68.1	115	2 PL0246	Ig heavy chain v r
19	429	68.0	123	2 PH1403	Ig heavy chain v r
20	424.5	67.3	107	2 PH1013	Ig heavy chain v r
21	419.5	66.5	118	2 G37267	Ig heavy chain v r
22	412.5	65.4	139	2 PS0024	Ig heavy chain pre
23	409.5	64.9	115	2 A54378	Ig heavy chain v r
24	409	64.8	138	2 S21810	Ig heavy chain v r
25	405.5	64.3	120	2 B22769	Ig heavy chain v r
26	405	64.2	246	2 S38950	Ig gamma chain - m
27	405	64.2	446	2 S40295	Ig gamma-2a chain
28	403.5	63.9	107	2 A27646	Ig heavy chain v r
29	402.5	63.8	116	2 S53751	antibody Fab Jel 1

30	402.5	63.8	139	1 MHMS18	Ig heavy chain pre
31	402.5	63.8	287	4 PC4402	pelB leader/Ig hea
32	400.5	63.5	120	2 S41394	Ig heavy chain v r
33	398.5	63.2	133	2 FC1155	Ig heavy chain pre
34	396.5	62.8	120	2 F28195	Ig heavy chain v r
35	396	62.8	136	2 PL0208	Ig heavy chain pre
36	395	62.6	119	2 D30562	Ig heavy chain v r
37	393.5	62.4	136	2 JL0077	Ig heavy chain pre
38	393.5	62.4	141	2 JL0076	Ig heavy chain pre
39	393.5	62.4	469	2 S37483	Ig gamma-2a chain
40	393	62.3	116	2 S55542	Ig heavy chain v r
41	393	62.3	131	2 A27472	Ig heavy chain pre
42	392.5	62.2	119	2 A24672	Ig heavy chain pre
43	392.5	62.2	120	2 G28195	Ig heavy chain v r
44	391	62.0	99	2 D37262	Ig heavy chain v r
45	391	62.0	99	2 C37262	Ig heavy chain v r

ALIGNMENTS

RESULT 1

S04576

Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000

C:Accession: S04576

R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.,

Eur. J. Immunol. 17, 91-95, 1987

A:Title: Molecular analysis of the murine lupus-associated anti-self response: Invol-

A:Reference number: S04573; MUID:87133856; PMID:3102255

A:Accession: S04576

A:Molecule type: mRNA

A:Residues: 1-136 <KOF>

A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PTD:g52030

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 509; DB 2; Length 136;

Best Local Similarity 82.9%; Pred. No. 1.4e-38;

Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYHHVWKQRPQGLEWIGWIDPENGDSGY 60

Db 20 EVQLQQSGAELVRPGASVKLSCTASGFNIDKDDYMHVWKQRPQGLEWIGWIDPENGDTQY 79

QY 61 APKFGQKATMTADSSNTAVYLQSLTSEDTAVYVCNAYYGDYEGYWGQGTITVTVSS 117

Db 80 ASKFGQKATMTADTSSNTVYLQSLTSEDTAVYVCYCTTGAYAMDYWGQGTISVTVSS 136

RESULT 2

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally id.

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 78.8%; Score 497.5; DB 2; Length 268;

Matches 83.1%; Pred. No. 3e-37;


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RESULT 7
S49220
Ig gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R:Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <KIP>
A:Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A:Experimental source: strain Balb/c
A:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-120/Domain: V region #status predicted <VRG>
F:121-221/Domain: C region #status predicted <CRG>
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 478; DB 2; Length 221;
Best Local Similarity 79.0%; Pred. No. 1.3e-35;
Matches 94; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVKLQSGAELVGSASVKLSCTASGFNIDTYMHVWKQRPQGLEWIGRIDPANGTKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 APKFOGKATMTADSSNTAYLQSLTSEDYAVYYC--NAYYGDYEGYWGQGTVTYVS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DPKFOGKATITADTSTNTAYLQSLTSEDYAVYYCVRRCYGSQEPYWGQGTTLTVSS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: S03471; S07453
R:Rocca-Serra, J.; Mazze, J.C.; Moinier, D.; Leciercq, L.; Somme, G.; Theze, J.; Fougere
EMBO J. 2, 867-872, 1983
A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A:Reference number: S03471; MUID:84057768; PMID:6416834
A:Accession: S03471
A:Molecule type: mRNA
A:Residues: 7-120 <ROC1>
A:Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A:Note: this sequence was determined from the differentiated gene
R:Rocca-Serra, J.; Mazze, J.C.; Moinier, D.; Leciercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A:Reference number: S07453; MUID:83058021; PMID:6815271
A:Accession: S07453
A:Molecule type: protein
A:Residues: 1-43 <ROC2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 475; DB 2; Length 120;
Best Local Similarity 79.0%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 15; Indels 2; Gaps 1;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLQSGAELVPGASVKLSCTASGFNIDTYMHVWKQRPQGLEWIGRIDPANGTKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 APKFOGKATMTADSSNTAYLQSLTSEDYAVYYC--GDYEGYWGQGTVTYVS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DPKFOGKATITADTSSNTAYLQSLTSEDYAVYYCARGWLRRDMDYWGQGTSTYVS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 9
S29594
Ig gamma chain (WM65) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S29594
R:Seymour, R.
submitted to the EMBL Data Library, February 1991
A:Reference number: S29593
A:Accession: S29594
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-178 <SEY>
A:Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C:Keywords: immunoglobulin

Query Match 74.4%; Score 469.5; DB 2; Length 178;
Best Local Similarity 78.3%; Pred. No. 6.1e-35;
Matches 94; Conservative 8; Mismatches 13; Indels 5; Gaps 2;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 14 EVQLQSGAELVPGASVKLSCTASGFNIDTYMHVWKQRPQGLEWIGRIDPANGYTEY 73
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 APKFOGKATMTADSSNTAYLQSLTSEDYAVYYC---NAYYGDYEGYWGQGTVTYVS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 74 DPKFOGKATITADTSTNTAYLQSLTSEDYAVYYCTGGNYAYG--MDYWGQGTSTYVS 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
S24289
Ig gamma chain V region (JS34/32) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S24289
R:Nonchamont, B.
submitted to the EMBL Data Library, September 1991
A:Description: Cloning and sequencing of the cDNA coding for the variable regions of
A:Reference number: S24287
A:Accession: S24289
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <MON>
A:Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 466; DB 2; Length 116;
Best Local Similarity 76.7%; Pred. No. 8.1e-35;
Matches 89; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 VKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGYA 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 VQLQSGAELVPGASVKLSCTASVFNIQDTYMHVWKQRPQGLEWIGRIDPANGNTHFD 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 PKFGKATMTADSSNTAYLQSLTSEDYAVYYCNAAYYGDYEGYWGQGTVTYVS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 PKFGKATITADTSSNTAYLQSLTSEDYAVYYCARWAGYFPDYWGQGTTLTVSS 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
A47271
nitrophenyl phosphate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
C:Species: synthetic
A:Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C>Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
C:Accession: A47271
R:Lesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A:Title: A genetic approach to the generation of antibodies with enhanced catalytic a
```

A:Reference number: A47271; MUID:93165660; PMID:8094556

A:Accession: A47271

A:Molecule type: DNA; protein

A:Residues: 1-114 <LES>

A:Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)

A:Note: parts of this sequence were determined by protein sequencing

F:22-96/Disulfide bonds: #status predicted

Query Match 73.6%; Score 464.5; DB 4; Length 114;
Best Local Similarity 77.8%; Pred. No. 1.1e-34;
Matches 9; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDSGY 60

Db 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGRIDPANVDYTKY 60

Qy 61 APKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYYDGYEGYWGQGTFTVYSS 117

Db 61 DPKEQDKATITADTSSKTYLQSLTSEDYAVYCNAYYDGYEGYWGQGTFTVYSS 114

RESULT 12

S06823

Ig heavy chain V region (clone IIC) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: S06823

R:Miller III, A.; Glasel, J.A.

J. Mol. Biol. 209, 763-778, 1989

A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp

A:Reference number: S06815; MUID:90064531; PMID:2555519

A:Accession: S06823

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-122 <MUI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 460.5; DB 2; Length 122;

Best Local Similarity 77.9%; Pred. No. 2.6e-34;

Matches 95; Conservative 8; Mismatches 14; Indels 5; Gaps 3;

Qy 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDSG 59

Db 1 EVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGRIDPANGNTK 60

Qy 60 YAPKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYY--GDYEG--YWGQGTFTVTV 115

Db 61 YPKFGKATITADTSSNTAYLQSLTSEDYAVYCNAYY--GDYEG--YWGQGTFTVTV 120

Qy 116 SS 117

Db 121 SS 122

RESULT 13

S03484

Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Variety: Strain BALB/c

C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000

C:Accession: S03484; S07453

R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Theze, J.; Fougereau, M.

EMBO J. 2, 867-872, 1983

A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT

hypervariable regions.

A:Reference number: S03471; MUID:84057768; PMID:6416834

A:Accession: S03484

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 10-120 <ROCI>

A:Cross-references: EMBL:X07144

A:Note: this sequence was determined from the differentiated gene

R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Theze, J.; Foug

J. Immunol. 129, 2554-2558, 1982

A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not

A:Note: parts of this sequence were determined by protein sequencing

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 454; DB 2; Length 120;
Best Local Similarity 75.6%; Pred. No. 9.9e-34;
Matches 90; Conservative 8; Mismatches 19; Indels 2; Gaps 1;

Qy 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDSGY 60

Db 1 EVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGRIDPANXNSKY 60

Qy 61 APKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYY--YGDYEGYWGQGTFTVYSS 117

Db 61 GPKFGKATITADTSSNTAYLQSLTSEDYAVYCNAYY--YGDYEGYWGQGTFTVYSS 119

RESULT 14

S03482

Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Variety: Strain BALB/c

C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000

C:Accession: S03482; S07453

R:Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,

EMBO J. 2, 867-872, 1983

A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-

hypervariable regions.

A:Reference number: S03471; MUID:84057768; PMID:6416834

A:Accession: S03482

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 10-115 <ROCI>

A:Cross-references: EMBL:X03219

A:Note: this sequence was determined from the differentiated gene

R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Theze, J.; Foug

J. Immunol. 129, 2554-2558, 1982

A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not

A:Note: parts of this sequence were determined by protein sequencing

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 453; DB 2; Length 115;

Best Local Similarity 76.5%; Pred. No. 1.2e-33;

Matches 88; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDSGY 60

Db 1 EVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGRIDPANGNTKY 60

Qy 61 APKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYYDGYEGYWGQGTFTVTV 115

Db 61 DPKFGKATITDSSNTAYLQSLTSEDYAVYCNAYYDGYEGYWGQGTFTVTV 115

RESULT 15

JC5322

p53 specific single-chain antibody Pab421 - human

C:Species: Homo sapiens (man)

C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C:Accession: JC5322

R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A>Title: Characterization of scFV-421, a single-chain antibody targeted to p53.
A:Reference number: JCS322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
C:Experimental source: hydricloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

	Query Match	71.6%;	Score 452;	DB 2;	Length 233;	
	Best Local Similarity	79.6%;	Pred. NO. 3e-33;			
	Matches	90;	Conservative	5;	Mismatches	14; Indels
					Gaps	1;
QY	5	QQSGAEILVGSGASVKLSCTTSGFNKIDFYHWHWKPQGLEIWIGDPNGDSGYAPXF	64			
	:	:: ::	:: :: ::	:	: :: ::	:
Dd	1	QESGAELVRSGASVKLSCTTSGFNINDYHWHWKKRPEQGLEIWRIGDIPENDGDMTRSS	60			
	:	:: ::	:: :: ::	:	: :: ::	:
QY	65	QGKATMTADSSNTAYLQLSSLTSEDTAVYYCNAYGDYEGYWGGQTFTTVSS	117			
	:	:: ::	:: :: ::	:	: :: ::	:
Dd	61	GVKATMTADTSNNTAYLQLSSLTSEDTAVYYCNAGM----DYWGQGTFTTVSS	109			
	:	:: ::	:: :: ::	:	: :: ::	:

Search completed: December 23, 2002, 07:31:38
Job time : 24.1279 secs

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Result No.	Query	Score	Match	Length	DB	ID	Description
1	402.5	63.8	139	1	HV03_MOUSE	P01751	mus musculus
2	389	61.6	120	1	HV03_MOUSE	P01747	mus musculus
3	384.5	60.9	137	1	HV11_MOUSE	P01755	mus musculus
4	380	60.2	140	1	HV02_MOUSE	P01746	mus musculus
5	377	59.7	117	1	HV12_MOUSE	P01756	mus musculus
6	373	59.1	138	1	HV48_MOUSE	P03980	mus musculus
7	368	58.3	117	1	HV13_MOUSE	P01757	mus musculus
8	368	58.3	136	1	HV15_MOUSE	P01759	mus musculus
9	365.5	57.9	120	1	HV50_MOUSE	P06329	mus musculus
10	363.5	57.6	147	1	HV1C_HUMAN	P01744	homo sapien
11	362.5	57.4	118	1	HV51_MOUSE	P06330	mus musculus
12	347	55.0	121	1	HV01_MOUSE	P01745	mus musculus
13	344	54.5	117	1	HV06_MOUSE	P01750	mus musculus
14	342	54.2	117	1	HV09_MOUSE	P01753	mus musculus
15	338	53.6	117	1	HV04_MOUSE	P01748	mus musculus
16	335	53.1	117	1	HV49_MOUSE	P06328	mus musculus
17	331	52.5	117	1	HV10_MOUSE	P01754	mus musculus
18	331	52.5	117	1	HV52_MOUSE	P06327	mus musculus
19	327	51.8	117	1	HV14_MOUSE	P01758	mus musculus
20	327	51.8	117	1	HV1B_HUMAN	P01743	homo sapien
21	324	51.3	117	1	HV05_MOUSE	P01749	mus musculus
22	322.5	51.1	119	1	HV40_MOUSE	P01810	mus musculus
23	320.5	50.8	119	1	HV37_MOUSE	P01807	mus musculus
24	315.5	50.0	114	1	HV00_MOUSE	P01741	mus musculus
25	313.5	49.7	119	1	HV38_MOUSE	P01808	mus musculus
26	311	49.3	117	1	HV42_MOUSE	P01812	mus musculus
27	308	48.8	117	1	HV1G_HUMAN	P23083	homo sapien
28	307.5	48.7	122	1	HV3G_HUMAN	P01768	homo sapien
29	307.5	48.7	136	1	HV16_MOUSE	P01783	mus musculus
30	305	48.3	142	1	HV0I_RAT	P01805	rattus norv
31	302	47.9	117	1	HV01_HUMAN	P01742	homo sapien
32	295	46.8	118	1	HV39_MOUSE	P01809	mus musculus
33	292	46.3	117	1	HV41_MOUSE	P01811	mus musculus

```

RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981);
RL Cell 24:625-637(1981);
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00539; AAA38172.1; -
CC PIR; A02038; G2MS43.
CC HSP; P01810; 2FBJ.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DOMAIN 118 122 D SEGMENT.
CC FT DOMAIN 123 137 JH2 SEGMENT.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON_TER 137 137
CC SQ SEQUENCE 137 AA; ADD5881BF44B8EC9 CRC64;

Query Match 60.9%; Score 384.5; DB 1; Length 137;
Best Local Similarity 63.6%; Pred. No. 1.3e-31;
Matches 75; Conservative 12; Mismatches 30; Indels 1; Gaps 1;

QY 1 QVKLQSGAEVLGSGASVKLSCTTSQFNKIDFVHWVKQRPQGLGWIGWIDPENGDSGY 60
Db 20 QVQLQPGAEFFKPGASVKLSCKASGYTFTSYLMHWVNPGRGLEWIGRIDPNSGTTY 79
QY 61 APKFGKATMTADSSNTAYLSLTSSTEDTAVYVCNAY-YGDYEGYWGQGTIVTSS 117
Db 80 NEHFRSKATLITDKPSSTAYMQLSSTSDSAVYCARYRLGRFYDYGQGTTLTSS 137

RESULT 4
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -----

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; J00493; AAA38128.1; -
DR PIR; A02028; HVM5G7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsenate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 60.2%; Score 380; DB 1; Length 140;
Best Local Similarity 60.7%; Pred. No. 3.7e-31;
Matches 74; Conservative 21; Mismatches 21; Indels 6; Gaps 3;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDPYMHVWQRPQGLEWIGIDPENGDSGY 60
DB 20 EVQLQSGAELVRAGSSVMSKASGYFTFTSYGHNWQRPQGLEWIGINPGNGYNY 79
QY 61 APKFOGKATMTADSSNTAYLQSLTSDTAVYVC---NAYYG---DYEGYWGQTTVTVV 115
DB 80 NEKFKGKTLTVDKSSSTAYMQLRLTSDTSASVYFCARSHYGGSYDFD-YWGQGTPLTV 138
QY 116 SS 117
DB 139 SS 140

RESULT 5
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 59.7%; Score 377; DB 1; Length 117;
Best Local Similarity 62.4%; Pred. No. 5.9e-31;
Matches 73; Conservative 14; Mismatches 30; Indels 0; Gaps 0;
QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDPYMHVWQRPQGLEWIGIDPENGDSGY 60
DB 1 EVQLQSGPELVKPGASVKMSKASGYFTFTSYGHNWQRPQGLEWIGIDIPNNGGTSY 60
QY 61 APKFOGKATMTADSSNTAYLQSLTSDTAVYVCNAYYCYEGYWGQTTVTVSS 117
DB 61 NOKFKGKATLTVDKSSSTAYMQLRLTSDTSASVYFCARSHYGGSYDFD-YWGQGTPLTVSS 117

RESULT 6

HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPIC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVM5T7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPIC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 127 FRAMEWORK-3.
FT DOMAIN 128 138 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 59.1%; Score 373; DB 1; Length 138;
Best Local Similarity 61.7%; Pred. No. 1.8e-30;
Matches 74; Conservative 16; Mismatches 26; Indels 4; Gaps 2;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDPYMHVWQRPQGLEWIGIDPENGDSGY 60
DB 20 QVQLQPGAEVLKPGASVQLSKASGHTFTNYWIHWKQRPQGLEWIGEIPNNGRSNY 79
QY 61 APKFOGKATMTADSSNTAYLQSLTSDTAVYVC---NAYYGYEGYWGQTTVTVSS 117
DB 80 NEKFKGKATLTVDKSSSTAYMQLRLTSDTSASVYFCARSHYGGSYDFD-YWGQGTPLTVSS 138

RESULT 7

HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

RESULT 10

HVIC_HUMAN
ID HVIC_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Mouldgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CELL PROTEIN.
DR PIR; A02026; EIHUND.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 57.6%; Score 363.5; DB 1; Length 147;
Best Local Similarity 51.6%; Pred. No. 1.7e-29;
Matches 66; Conservative 24; Mismatches 27; Indels 11; Gaps 2;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
DB 20 QFOLVQSGAEVRKPGASVRKSCAGYTIDSYIHWRQAPGHLEWGWINPNSGGTNY 79
QY 61 APKFOGKATMTADSSNTAYLQLSLTSDEDTAVYYC---NAYYGDYEGY-----WGQ 109
DB 80 APFQGRVMTDRDASFTAYMDLSRLSDSDSAVFYCAKSDPFWSDYNFDSYTLTDVWGQ 139
QY 110 GTTIVTSS 117
DB 140 GTTIVTSS 147

RESULT 11

HVS1_MOUSE
ID HVS1_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 57.4%; Score 362.5; DB 1; Length 118;
Best Local Similarity 59.7%; Pred. No. 1.7e-29;
Matches 71; Conservative 17; Mismatches 28; Indels 3; Gaps 2;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
DB 1 EVOLOQSGPELVKPGASVRKSCAGYTFTDYIMNVKQSHGKSLWIGDINPNNGTGY 60
QY 61 APKFOGKATMTADSSNTAYLQLSLTSDEDTAVYYCNAVYGDYEGY--WGQTTIVTSS 117
DB 61 NOKFKGKATLTVDKSSATYMLRSLTSDSAVYVCARGYG-YDPPDVMTGTIVTSS 118

RESULT 12

HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zukut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zukut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 55.0%; Score 347; DB 1; Length 121;
Best Local Similarity 56.2%; Pred. No. 6.1e-28;

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DT 01-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR; B02034; HYMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match 54.2%; Score 342; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 1.8e-27;
Matches 64; Conservative 13; Mismatches 19; Indels 0; Gaps

QY 1 QVQLQQSGAELVSGASVKLSCTTSGFNIKDFYHHWVKRPEQGLEWIGWIDPENGDSGY 60
Db 20 QVQLQQGAELVPGASVKLSCKASGYFTSYHHWVKRPGRGLEWIGRIDPNSSGTTY 115
QY 61 APFQGGKATWDSSNTAYLQLSLTSDTAYTVC 96
Db 80 NEKFKSKATITVDTSSSTAYMQLSLTSDSAVYVC 115

RESULT 15
HV04_MOUSE STANDARD; PRT; 117 AA.
ID AC P01748;
IC HV04_MOUSE STANDARD; PRT; 117 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

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DR PIR; A02030; HVMS23.
DR HSP; P01810; 2FRJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 53.6%; Score 338; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 4.6e-27;
Matches 64; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVGGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDGSGY 60
Db 20 QVQLQPGTGLVKGASVKLSCKASGYTFYSYMHVVKORPGQGLEWIGNINPGNGGTNY 79

QY 61 APKEQKATMTADSSNTAYLQLSLTSEDYAVYC 96
Db 80 NEKFKSVTLTVDKSSSTAYTQLSLTSDSAVYC 115

Search completed: December 23, 2002, 07:26:11
Job time : 12.564 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 48.5233 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-7

Perfect score: 631

Sequence: 1 QVKLQSGAELVGSASVKL.....AYYGDYEGYWGQGTIVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organalle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	80.7	468	11 Q99L31	Q99L31 mus musculus
2	427	67.7	109	11 Q9JL85	Q9JL85 mus musculus
3	410.5	65.1	143	11 Q924P9	Q924P9 mus musculus
4	406	64.3	146	11 Q924R8	Q924R8 mus musculus
5	402.5	63.8	145	11 Q924Q7	Q924Q7 mus musculus
6	402	63.7	146	11 Q924Q3	Q924Q3 mus musculus
7	400.5	63.5	118	11 Q921C4	Q921C4 mus musculus
8	399.5	63.3	473	11 Q99L25	Q99L25 mus musculus
9	399	63.2	473	11 Q9D8L4	Q9D8L4 mus musculus
10	397.5	63.0	143	11 Q924R0	Q924R0 mus musculus
11	397.5	63.0	143	11 Q924Q5	Q924Q5 mus musculus
12	397	62.9	140	11 Q924R2	Q924R2 mus musculus
13	396	62.8	142	11 Q924Q1	Q924Q1 mus musculus
14	394.5	62.5	145	11 Q924R4	Q924R4 mus musculus
15	393.5	62.4	145	11 Q924R1	Q924R1 mus musculus
16	390.5	61.9	143	11 Q91V67	Q91V67 mus musculus

17	390.5	61.9	145	11	Q924Q9	Q924Q9 mus musculus
18	390	61.8	144	11	Q924P5	Q924P5 mus musculus
19	389.5	61.7	137	11	Q924S6	Q924S6 mus musculus
20	389.5	61.7	145	11	Q924Q6	Q924Q6 mus musculus
21	388.5	61.6	143	11	Q924P6	Q924P6 mus musculus
22	387	61.3	142	11	Q924Q2	Q924Q2 mus musculus
23	386.5	61.3	143	11	Q924R7	Q924R7 mus musculus
24	386	61.2	140	11	Q924P8	Q924P8 mus musculus
25	386	61.2	481	11	Q91WT1	Q91WT1 mus musculus
26	385.5	61.1	141	11	Q924Q4	Q924Q4 mus musculus
27	385.5	61.1	145	11	Q924P7	Q924P7 mus musculus
28	384.5	60.9	145	11	Q924R3	Q924R3 mus musculus
29	382.5	60.6	139	11	Q924R5	Q924R5 mus musculus
30	381.5	60.5	143	11	Q91VA2	Q91VA2 mus musculus
31	381	60.4	117	11	Q9QXF0	Q9QXF0 mus musculus
32	379	60.1	489	11	Q8VCX4	Q8VCX4 mus musculus
33	378.5	60.0	278	11	Q921K1	Q921K1 mus musculus
34	378.5	60.0	613	11	Q8VCX7	Q8VCX7 mus musculus
35	377	59.7	117	11	Q9QXE9	Q9QXE9 mus musculus
36	375	59.4	146	11	Q924Q8	Q924Q8 mus musculus
37	374	59.3	168	11	Q8VDC9	Q8VDC9 mus musculus
38	373	59.1	474	11	Q8R3H6	Q8R3H6 mus musculus
39	372.5	59.0	143	11	Q924Q0	Q924Q0 mus musculus
40	369.5	58.6	109	11	Q9JL75	Q9JL75 mus musculus
41	368	58.3	147	11	Q925S3	Q925S3 mus musculus
42	367	58.2	170	11	Q925S2	Q925S2 mus musculus
43	367	58.2	481	11	Q91WT3	Q91WT3 mus musculus
44	363.5	57.6	463	11	Q99LC4	Q99LC4 mus musculus
45	362.5	57.4	124	4	Q9UL92	Q9UL92 homo sapien

ALIGNMENTS

RESULT 1

Q99L31 PRELIMINARY; PRT; 468 AA.

AC Q99L31:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003878; AA03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig_c1; 3.
DR SMART; SM00406; Ig_v; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match: 80.7%; Score 509; DB 11; Length 468;

Best Local Similarity 80.7%; Pred. No. 7.1e-43;

Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSGY 60

Db 20 EVQLQSGAELVPGASVKLSCTSGFNKDKSLMHVVKORPEQGLEWIGWIDPDEGETKY 79

[illegible]

QY	1	QVRLQOQGAELVSGASVKLSCTTSGFNIRKDFYMHVWKQRPQGLEWIGWIDPENGDSGY	60
QY	1		60
Db	1	QVQLQOQGAELVPGASVKLSRASGYFTSYMHVWKQRPQGRGLEWIGRIDPNSGSKY	60
QY	61	APRFQGRATMTADSSNSTAYLQISSLTSEDATAYYC-NAYGD---YEGYWGCGTTVTVS	116
QY	61		116
Db	61	NEKFSKATLTVDKPSSTAYMQISSLTSEDSAVYYCARSYGSSLYFYDWGCGTTLTVS	120
QY	117	S 117	
Db	121	S 121	
RESULT 5			
Q924Q7		PRELIMINARY;	
ID	Q924Q7	PRT;	145 AA.
AC	Q924Q7;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	VHL86.2-D-J-C mu protein (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 63.8%; Score 402.5; DB 11; Length 145;
Best Local Similarity 65.8%; Pred. No. 8.1e-33;
Matches 79; Conservative 13; Mismatches 25; Indels 3; Gaps 2;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGDSGY 60
Db 1 QVQLQPGAELVKPGASVKLSCKASGYTFTSYMHVWKORPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFOGKATMTADSSNTAYLQSLTSEDYAVYICNA--YIG-DYEGYWGQGTITVSS 117
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLSITSEDSAVYICARYDYIGSSYFDYWGQGTITVSS 120

RESULT 6
Q924Q3 PRELIMINARY; PRT; 146 AA.
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RL Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067797; BAB63282.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 63.7%; Score 402; DB 11; Length 146;
Best Local Similarity 66.1%; Pred. No. 9.2e-33;
Matches 80; Conservative 14; Mismatches 23; Indels 4; Gaps 3;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGDSGY 60
Db 1 QVQLQPGAELVKPGASVKLSCKASGYTFTSYMHVWKORPGRGLEWIGRIDPNSGGTKY 60

QY 61 APKFOGKATMTADSSNTAYLQSLTSEDYAVYIC--NAY-YGDYE-GYWGQGTITVSS 116
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLSITSEDSAVYICARSLYDYGDMYWGQGTITVSS 120

QY 117 S 117
Db 121 S 121
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RESULT 7
Q921C4 PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR HSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 63.5%; Score 400.5; DB 11; Length 118;
Best Local Similarity 66.1%; Pred. No. 1e-32;
Matches 78; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGDSGY 60
Db 1 QVQVQSGAELARPWASVKLSCKASGYNFNSYMQVWKORPQGLEWICAIYPGDGTSY 60

QY 61 APKFOGKATMTADSSNTAYLQSLTSEDYAVYIC--NAYYGDYEGYWGQGTITVSS 117
Db 61 TQKFRGKATLTADKSSSTAYMQLSLSITSEDSAVYICARTVGGYFDYWGQGTITVSS 118

RESULT 8
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cdna 1810600009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA003888.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SQ SEQUENCE 473 AA; 52449 MW; BE9898B7986DA155 CRC64;
Query Match 63.3%; Score 399.5; DB 11; Length 473;
Best Local Similarity 63.7%; Pred. No. 7e-32;
Matches 79; Conservative 16; Mismatches 22; Indels 7; Gaps 2;
QY 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
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QY 61 APKFGKATMTADSSNTAYLQSLTSEDVAVYVC-----NAYYG---DYGGYWGQGT 113
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QY 114 TVSS 117
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Db 140 TVSS 143
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ID Q9D8L4
AC Q9D8L4; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 18100600909rik protein.
GN IGH-1 ORF18100600909RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons Pa., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordonepp., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Igh-1.
DR InterPro; IPR003597; Igh-cl.
DR InterPro; IPR003600; Igh-like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh-v.
DR Pfam; PF00047; Igh; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Query Match 63.2%; Score 399; DB 11; Length 473;

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Best Local Similarity 64.7%; Pred. No. 7.9e-32;
Matches 77; Conservative 18; Mismatches 22; Indels 2; Gaps 1;
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   ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 APKFGKATMTADSSNTAYLQSLTSEDVAVYVC--NAYYGYEGYWGQGTVTYVSS 117
   ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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ID Q924R0
AC Q924R0; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067790; BAB63275.1; -.
DR InterPro; IPR003598; Ig_c2.
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DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
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FT NON_TER 1
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Query Match 63.0%; Score 397.5; DB 11; Length 143;
Best Local Similarity 65.3%; Pred. No. 2.5e-32;
Matches 77; Conservative 14; Mismatches 26; Indels 1; Gaps 1;
QY 1 QVQLQSGAEVLGSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSGY 60
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Db 1 QVQLQSGAEVLKPGASVKISCKASGYFTTFSYWHVWKQRPQGLEWIGRIDPNSGSKY 60
   ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 APKFGKATMTADSSNTAYLQSLTSEDVAVYVCNAYYGYE-GYWGQGTVTYVSS 117
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RESULT 11
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ID Q924Q5
AC Q924Q5; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
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AC Q924R1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-DEJ-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y, Kozono H, Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067789; BAB63274.1; -
DR InterPro; IPR03006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match: 62.4%; Score 393.5; DB 11; Length 145;
Best Local Similarity 64.2%; Pred. No. 6.5e-32;
Matches 77; Conservative 13; Mismatches 27; Indels 3; Gaps 1;

Qy 1 QVQZQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKRPEQGLEWIGWIDPENGDSGY 60
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Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDPAVYCNAYYCD---YEGYWGQGTITVYSS 117
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Search completed: December 23, 2002, 07:29:55
Job time : 49.5233 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 : Search time 19.4651 Seconds
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Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIELTQSPALMSASPGKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext.0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	541	97.0	108	US-09-171-945-9	Sequence 9, Appl
2	539	96.6	235	US-09-171-945-17	Sequence 17, Appl
3	534	95.7	129	US-08-116-778E-2	Sequence 2, Appl
4	534	95.7	129	US-08-438-562-2	Sequence 2, Appl
5	534	95.7	129	US-08-483-528B-92	Sequence 92, Appl
6	532	95.3	270	US-08-652-507-2	Sequence 2, Appl
7	532	95.3	553	US-08-661-052-16	Sequence 16, Appl
8	532	95.3	553	US-09-188-082-16	Sequence 16, Appl
9	532	95.3	553	US-09-364-088-16	Sequence 16, Appl
10	532	95.3	553	US-09-102-716-16	Sequence 16, Appl
11	526	94.3	281	US-09-423-439-44	Sequence 44, Appl
12	526	94.3	666	US-09-423-439-51	Sequence 51, Appl
13	518	92.8	105	US-08-434-000A-12	Sequence 12, Appl
14	518	92.8	105	US-09-312-157-12	Sequence 12, Appl
15	516	92.5	106	US-07-634-278-1	Sequence 1, Appl
16	516	92.5	106	US-07-634-278-16	Sequence 16, Appl
17	516	92.5	106	US-08-477-728-1	Sequence 1, Appl
18	516	92.5	106	US-08-477-728-16	Sequence 16, Appl
19	516	92.5	106	US-08-474-040-1	Sequence 1, Appl
20	516	92.5	106	US-08-474-040-16	Sequence 16, Appl
21	516	92.5	106	US-08-487-200-1	Sequence 1, Appl
22	516	92.5	106	US-08-487-200-16	Sequence 16, Appl
23	516	92.5	106	US-08-488-113B-163	Sequence 163, Appl
24	516	92.5	106	US-08-477-484B-163	Sequence 163, Appl
25	516	92.5	106	US-08-107-669D-49	Sequence 49, Appl
26	516	92.5	106	US-08-472-788A-83	Sequence 83, Appl
27	516	92.5	106	US-08-477-531B-49	Sequence 49, Appl

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29	516	92.5	106	2	US-08-082-842A-83	Sequence 83, Appl
30	516	92.5	106	4	US-08-839-765-163	Sequence 163, App
31	516	92.5	106	4	US-09-136-389-163	Sequence 163, App
32	516	92.5	106	4	US-08-484-537-1	Sequence 1, Appl
33	516	92.5	106	4	US-08-484-537-16	Sequence 16, Appl
34	516	92.5	106	4	US-09-610-838-163	Sequence 163, App
35	516	92.5	239	3	US-08-279-772A-8	Sequence 8, Appl
36	516	92.5	239	1	US-08-902-486-11	Sequence 11, Appl
37	516	92.5	599	1	US-08-463-163-3	Sequence 3, Appl
38	498	89.2	130	4	US-09-393-385B-113	Sequence 113, App
39	495	88.7	130	4	US-09-393-385B-111	Sequence 111, App
40	490	87.8	246	1	US-08-469-486-57	Sequence 57, Appl
41	490	87.8	246	2	US-08-469-658-57	Sequence 57, Appl
42	489	87.6	128	4	US-08-619-491-2	Sequence 2, Appl
43	489	87.6	128	5	PCT-US95-07302-2	Sequence 2, Appl
44	486	87.1	107	1	US-08-211-202-3	Sequence 3, Appl
45	483	86.6	244	2	US-08-553-497A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-171-945-9
: Sequence 9, Application US/09171945
: Patent No. 6277599
: GENERAL INFORMATION:
: APPLICANT: Emery, Stephen
: APPLICANT: Copley, Clive Graham
: APPLICANT: Edge, Michael Derek
: TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
: TITLE OF INVENTION: Antibody and Their Therapeutic Use in an Adept System
: FILE REFERENCE: Monoclonal Antibody to CEA
: CURRENT APPLICATION NUMBER: US/09/171,945
: PRIOR FILING DATE: 1998-10-29
: PRIOR APPLICATION NUMBER: GB9703103.3
: PRIOR FILING DATE: 1997-02-14
: PRIOR APPLICATION NUMBER: GB9609405.7
: PRIOR FILING DATE: 1996-05-04
: PRIOR APPLICATION NUMBER: PCT/GB97/01165
: PRIOR FILING DATE: 1997-04-29
: NUMBER OF SEQ ID NOS: 131
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 9
: TYPE: PRT
: LENGTH: 108
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-9

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QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
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RESULT 2

US-09-171-945-17
: Sequence 17, Application US/09171945
: Patent No. 6277599
: GENERAL INFORMATION:
: APPLICANT: Emery, Stephen
: APPLICANT: Copley, Clive Graham
: APPLICANT: Edge, Michael Derek


```

CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-483-528B-92
Query Match 95.7%; Score 534; DB 2; Length 129;
Best Local Similarity 97.2%; Pred. No. 7.3e-41;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 IELTQSPAINASDPGEKVTTTCSASSVSVMHWFOQKPGTSPKLIWYSTNLASGVPARF 61
Db 24 IVLTQSPAINASDPGEKVTTTCSASSVSVMHWFOQKPGTSPKLIWYSTNLASGVPARF 83
QY 62 SSGSGGTSYSLTISRMEADAATYYCOORSSYPETFGSGTKLEIKR 107
Db 84 SSGSGGTSYSLTISRMEADAATYYCOORSSYPYTFGGGTKLEIKR 129
RESULT 6
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
; GENERAL INFORMATION:
; APPLICANT:

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TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-652-507#2
; Query Match 95.3%; Score 532; DB 2; Length 270;
; Best Local Similarity 97.1%; Pred. No. 2.4e-40;
; Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; QY 4 LTQSPAIMSASGPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARFSG 63
; DB 165 LTQSPAIMSASGPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARFSG 224
; QY 64 SGGTSTSYSLTISRMEADAATYYCQORSSYPFTFGAGTKLEIKRA 108
; DB 225 SGGTSTSYSLTISRMEADAATYYCQORSSYPFTFGAGTKLEIKRA 269
; RESULT 7
; US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; APPLICATION NUMBER: US/08/661,052

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
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; LENGTH: 553 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-661-052-16
; Query Match 95.3%; Score 532; DB 2; Length 553;
; Best Local Similarity 97.1%; Pred. No. 5.3e-40;
; Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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; DB 415 LTQSPAIMSASGPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARFSG 474
; QY 64 SGGTSTSYSLTISRMEADAATYYCQORSSYPFTFGAGTKLEIKRA 108
; DB 475 SGGTSTSYSLTISRMEADAATYYCQORSSYPFTFGAGTKLEIKRA 519
; RESULT 8
; US-08-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; APPLICATION NUMBER: US/09/188,082

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-16

Query Match 95.3%; Score 532; DB 4; Length 553;
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 63
Db 415 LTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 474

QY 64 SSGTYSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA 108
Db 475 SSGTYSYSLTISRMEADAATYCCQORSSYPFTFGAGTKLEIKRA 519

RESULT 9
US-09-364-088-16
; Sequence 16, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-16

Query Match 95.3%; Score 532; DB 4; Length 553;
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 63
Db 415 LTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 474

QY 64 SSGTYSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA 108
Db 475 SSGTYSYSLTISRMEADAATYCCQORSSYPFTFGAGTKLEIKRA 519
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RESULT 10
US-09-102-716-16
; Sequence 16, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Cheilan Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 95.3%; Score 532; DB 4; Length 553;
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 63
Db 415 LTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 474

QY 64 SSGTYSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA 108
Db 475 SSGTYSYSLTISRMEADAATYCCQORSSYPFTFGAGTKLEIKRA 519

RESULT 11
US-09-423-439-44
; Sequence 44, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
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Best Local Similarity 93.3%; Pred. No. 1.6e-39; Indels 0; Gaps 0;
Matches 98; Conservative 4; Mismatches 3;

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Db 1 DIVMTQSPALMSASPEKVTITCSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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QY 61 FSGSGGTSYSTISRMEADAATYCCQORSYPYTFGSGTKLEI 105
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RESULT 14

US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-351
; SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Guy's 13 Kappa
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-312-157-12

Query Match 92.8%; Score 518; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 1.6e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIETQSPALMSASPEKVTITCSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
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Db 1 DIVMTQSPALMSASPEKVTITCSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
||:|||||
QY 61 FSGSGGTSYSTISRMEADAATYCCQORSYPYTFGSGTKLEI 105
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Db 61 FSGSGGTSYSTISRMEADAATYCHQRTSYPTFGGTKLEI 105
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RESULT 15

US-07-634-278-1
; Sequence 1, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..106
; OTHER INFORMATION: /note= "Variable region of the mouse
; anti-Tac antibody light chain."
US-07-634-278-1

Query Match 92.5%; Score 516; DB 1; Length 106;
Best Local Similarity 93.3%; Pred. No. 2.4e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db 2 IYLTQSPALMSASPEKVTITCSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPAR 61
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QY 62 SGSGSGTSYSTISRMEADAATYCCQORSYPYTFGSGTKLEIK 106
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Db 62 SGSGSGTSYSTISRMEADAATYCHQRTSYPTFGSGTKLEIK 106
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Search completed: December 23, 2002, 07:33:18
Job time : 20.4651 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 10.0465 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIELTQSPAINASPGKVT.....QRSSYPFFGSGTKLEIKRA 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	558	100.0	108	10	US-09-865-198-8
3	558	100.0	240	10	US-09-976-787-28
4	558	100.0	240	10	US-09-865-198-27
5	549	98.4	106	10	US-09-976-787-24
6	549	98.4	106	10	US-09-865-198-23
7	549	98.4	238	10	US-09-976-787-29
8	549	98.4	238	10	US-09-865-198-28
9	541	97.0	108	10	US-09-910-059-9
10	539	96.6	235	10	US-09-910-059-17
11	523	93.7	669	9	US-09-807-721-2
12	518	92.8	105	9	US-09-982-107-12
13	509	91.2	107	9	US-09-144-886-88
14	506	90.7	119	10	US-09-808-037-28
15	506	90.7	239	10	US-09-808-037-6
16	505	90.5	107	9	US-09-144-886-76
17	500	89.6	107	9	US-09-144-886-90
18	489	87.6	107	9	US-09-144-886-75
19	489	87.6	107	9	US-09-144-886-78

20	484	86.7	107	9	US-09-144-886-82	Sequence 82, Appl
21	484	86.7	107	9	US-09-144-886-83	Sequence 83, Appl
22	484	86.7	109	9	US-09-144-886-91	Sequence 91, Appl
23	483	86.6	131	10	US-09-881-823-6	Sequence 6, Appl
24	479.5	85.9	112	9	US-09-144-886-89	Sequence 86, Appl
25	471	84.4	109	9	US-09-144-886-96	Sequence 96, Appl
26	466	83.5	107	10	US-09-965-099-11	Sequence 11, Appl
27	466	83.5	107	12	US-10-051-852-11	Sequence 11, Appl
28	466	83.5	109	9	US-09-144-886-79	Sequence 79, Appl
29	466	83.5	112	10	US-09-965-099-103	Sequence 103, App
30	466	83.5	112	12	US-10-051-852-103	Sequence 103, App
31	465	83.3	109	9	US-09-144-886-97	Sequence 97, Appl
32	463	83.0	106	10	US-09-158-120A-35	Sequence 35, Appl
33	461	82.6	106	10	US-09-965-099-105	Sequence 105, App
34	461	82.6	106	12	US-10-051-852-105	Sequence 105, App
35	459	82.3	109	9	US-09-144-886-77	Sequence 77, Appl
36	459	82.3	109	9	US-09-144-886-98	Sequence 98, Appl
37	458	82.1	107	10	US-09-910-059-71	Sequence 71, Appl
38	458	82.1	235	10	US-09-910-059-99	Sequence 99, Appl
39	449	80.5	127	10	US-09-753-436-80	Sequence 80, Appl
40	448	80.3	106	10	US-09-893-615-89	Sequence 89, Appl
41	447	80.1	107	10	US-09-910-059-61	Sequence 61, Appl
42	445	79.7	107	10	US-09-910-059-50	Sequence 50, Appl
43	445	79.7	235	10	US-09-910-059-52	Sequence 52, Appl
44	442	79.2	109	9	US-09-144-886-92	Sequence 92, Appl
45	437	78.3	107	10	US-09-910-059-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match	100.0%	Score 558;	DB 10;	Length 108;
Best Local Similarity	100.0%;	Pred. No. 1.7e-31;		
Matches 108;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DIELTQSPAINASPGKVTITCSASSSVSMHFWQKPGTSPKLIWYTSNLSASGYPAR	60	
Db	1	DIELTQSPAINASPGKVTITCSASSSVSMHFWQKPGTSPKLIWYTSNLSASGYPAR	60	
QY	61	FGSGSGTGYSLTISRMEADAATYCCQQRSSYPFFTGSGTKLEIKRA	108	
Db	61	FGSGSGTGYSLTISRMEADAATYCCQQRSSYPFFTGSGTKLEIKRA	108	

RESULT 2

US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping

; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US 09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match
Best Local Similarity 100.0%; Score 558; DB 10; Length 108;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 60
Db 1 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 60
Qy 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 108
Db 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 108

RESULT 3
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28

Query Match
Best Local Similarity 100.0%; Score 558; DB 10; Length 240;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 133 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 192
Qy 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 108
Db 193 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 240

RESULT 4
US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102

; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27

Query Match
Best Local Similarity 100.0%; Score 558; DB 10; Length 240;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 60
Db 133 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 192
Qy 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 108
Db 193 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 240

RESULT 5
US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match
Best Local Similarity 98.4%; Score 549; DB 10; Length 106;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 60
Db 1 DIELTQSPAINASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSASGVAP 60
Qy 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIK 106
Db 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIK 106

RESULT 6
US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749

; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 98.4%; Score 549; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
|||||
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 106
|||||
DB 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 106

RESULT 7

US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 98.4%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
|||||
DB 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 192
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 106
|||||
DB 193 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 238

RESULT 8

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 98.4%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
|||||
DB 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 192
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 106
|||||
DB 193 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 238

RESULT 9

US-09-910-059-9
; Sequence 9, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-9

Query Match 97.0%; Score 541; DB 10; Length 108;
Best Local Similarity 95.4%; Pred. No. 2.3e-30;
Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
|||||
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIKRA 108
|||||
DB 61 FSGSGSGTSYSLTISRMEADAATYYCQORSTYPLTFFGAGTKLEIKRA 108

RESULT 10

US-09-910-059-17
; Sequence 17, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059

; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric light chain sequence
US-09-910-059-17

Query Match 96.6%; Score 539; DB 10; Length 235;
Best Local Similarity 96.3%; Pred. No. 5.6e-30;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 23 DIETQSPAIMSASPGKVTITCSASSSVTYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 82
Qy 61 FSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
Db 83 FSGSGSTSYSLTISRMEADAATYYCQQRSTYPLTFGAGTKLEIKR 129

RESULT 11
US-09-807-721-2
; Sequence 2, Application US/09807721
; Patent No. US20020174453A1
; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,721
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-721-2

Query Match 93.78%; Score 523; DB 9; Length 669;
Best Local Similarity 92.5%; Pred. No. 1.4e-28;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 457 DIVTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 516
Qy 61 FSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
Db 517 FSGSGSTSYSLTISRMEADAATYYCHQRTSYPTTFGGGKLEIKR 563

RESULT 12
US-09-982-107-12
; Sequence 12, Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.

; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 kappa
US-09-982-107-12

Query Match 92.88%; Score 518; DB 9; Length 105;
Best Local Similarity 93.3%; Pred. No. 7.7e-29;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 1 DIVTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Qy 61 FSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 105
Db 61 FSGSGSTSYSLTISRMEADAATYYCHQRTSYPTTFGGGKLEI 105

RESULT 13
US-09-144-886-88
; Sequence 88, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bont/a clone
; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88

Query Match 91.2%; Score 509; DB 9; Length 107;
Best Local Similarity 97.0%; Pred. No. 3.1e-28;
Matches 97; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Qy 61 FSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSG 100
Db 61 FSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGG 100

RESULT 14
US-09-808-037-28
; Sequence 28, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

```
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 119
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-808-037-28

Query Match          90.7%; Score 506; DB 10; Length 119;
Best Local Similarity 90.6%; Pred. NO. 5.3e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGCKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSGVPAR 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 14 DIELTQSPAIMSASPGCKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSGVPAR 73
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FSGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 74 FSGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGGGAKLEIK 119
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 15
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6

Query Match          90.7%; Score 506; DB 10; Length 239;
Best Local Similarity 90.6%; Pred. No. 9e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGCKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSGVPAR 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 134 DIELTQSPAIMSASPGCKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSGVPAR 193
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FSGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 194 FSGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGGGAKLEIK 239
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: December 23, 2002, 07:58:20
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OM protein - protein search, using sw model

Run On: December 23, 2002, 07:17:57 ; Search time 21.3488 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-8
Perfect score: 558
Sequence: 1 DIETQSPAINASPGKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	517	92.7	140	2 PL0013	Ig kappa chain pre
2	513	91.9	106	2 B54378	Ig light chain v r
3	492	88.2	132	2 S05268	Ig kappa chain pre
4	487	87.3	107	2 PC4405	Ig kappa chain v r
5	486	87.1	99	2 D38601	Ig kappa chain v r
6	483	86.6	130	2 A32513	Ig kappa chain pre
7	481	86.2	107	2 A30562	Ig kappa chain v r
8	476	85.3	107	2 B30562	Ig kappa chain v r
9	474	84.9	106	2 G27887	Ig kappa chain v r
10	473	84.8	130	1 JL0079	Ig kappa chain pre
11	472	84.6	106	2 PS0070	Ig kappa chain v r
12	470	84.2	105	2 S26338	Ig kappa chain v r
13	466	83.5	120	2 S66536	Ig light chain v r
14	465	83.3	103	2 S29591	Ig kappa chain v r
15	465	83.3	107	2 PD0011	Ig kappa chain v r
16	465	83.3	108	2 PL0278	Ig kappa chain v r
17	464.5	83.2	108	2 G30560	Ig kappa chain v r
18	463	83.0	106	2 PS0071	Ig kappa chain v r
19	461	82.6	104	2 B49049	Ig kappa chain v r
20	461	82.6	108	2 PL0276	Ig kappa chain v r
21	461	82.6	108	2 PL0277	Ig kappa chain v r
22	460	82.4	235	2 S25058	Ig kappa chain - m
23	458	82.1	91	2 S17626	Ig kappa chain v r
24	455	81.5	107	2 A42848	Ig light chain v r
25	455	81.5	107	2 PT0406	Ig kappa chain v r
26	455	81.5	130	2 B32456	Ig kappa chain pre
27	453	81.2	107	2 S11119	Ig kappa chain v r
28	453	81.2	108	2 PS0069	Ig kappa chain v r
29	453	81.2	123	2 S05269	Ig kappa chain pre

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30 451.5 80.9 108 2 S38720 Ig light chain v r
31 451 80.8 107 2 S11118 Ig kappa chain v r
32 450 80.6 91 2 S17630 Ig kappa chain v r
33 450 80.6 104 2 JC6076 anti-b-dimer monoc
34 448 80.3 107 2 PT0401 Ig light chain v r
35 448 80.3 120 2 A34871 Ig kappa chain v r
36 446 79.9 100 2 S29590 Ig kappa chain v r
37 446 79.9 107 2 PT0398 Ig light chain v r
38 446 79.9 108 2 S29581 Ig kappa chain v r
39 446 79.9 130 2 S04573 Ig kappa chain pre
40 445 79.7 107 2 S11121 Ig kappa chain v r
41 442 79.2 107 2 PT0402 Ig light chain v r
42 441 79.0 106 2 PL0082 Ig kappa chain v r
43 441 79.0 107 2 PT0403 Ig light chain v r
44 440 78.9 97 2 S26341 Ig light chain v r
45 440 78.9 113 2 S03410 Ig kappa chain pre
```

ALIGNMENTS

RESULT 1

PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PL0013

R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-idiotypic antibodies.

A:Reference number: PL0011; MUID:88142863; PMID:3125424

A:Accession: PL0013

A:Molecule type: mRNA

A:Residues: 1-140 <CHE>

A:Experimental source: cell line 4C11

C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-42/Domain: signal sequence #status predicted <SIG>

F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F:38-111/Domain: immunoglobulin homology <IMM>

F:46-55/Region: complementarity-determining 1

F:71-77/Region: complementarity-determining 2

F:110-118/Region: complementarity-determining 3

F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 92.7%; Score 517; DB 2; Length 140;
Best Local Similarity 94.4%; Pred. No. 4.3e-35;
Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IELTQSPAINASPGKVTITCSASSSVSMHWFQOKPGTSPKLIWYTSNLSAGVPAKF 61

DB 24 IVLTQSPAINASPGKVTITCSASSSVSMHWFQOKPGTSPKLIWYTSNLSAGVPAKF 83

QY 62 SSGSGTSTSLTISRMEADAATYTCQQRSSYPFTFGSGTKLEIKRA 108

DB 84 SSGSGTSTSLTISRMEADAATYTCQQRSSYPFTFGSGTKLEIKRA 130

RESULT 2

B54378

Ig light chain V region anti-triplex DNA - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B54378

R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluor

A:Reference number: A54378; MUID:94165109; PMID:7509814

A:Accession: B54378

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-106 <AGA>

A;Cross-references: GB:S68985; NID:g545746; PIDN:AA30096.1; PID:g545747
 A;Experimental source: spleen and myeloma cell line MOPC 315.43
 A;Note: sequence inconsistent with nucleotide translation
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 91.9%; Score 513; DB 2; Length 106;
 Best Local Similarity 94.3%; Pred. No. 7.1e-35;
 Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPAR 61
 Db 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPAR 61

Qy 62 SGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIK 106
 Db 62 SGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGAGTKLEIK 106

RESULT 3

S05268
 Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
 C;Accession: S05268; J10062; S03846
 R;Levy, S.

Submitted to the EMBL Data Library, February 1989

A;Reference number: S05267

A;Accession: S05268

A;Molecule type: mRNA

A;Residues: 1132 <LEV>

A;Cross-references: EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261

R;Carroll, W.; Starnes, C.O.; Levy, R.; Levy, S.

J. Exp. Med. 168, 1607-1620, 1988

A;Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explanation

A;Reference number: J10061; MUID:89035985; PMID:3141553

A;Accession: J10062

A;Molecule type: mRNA

A;Residues: 12120 <CAR>

A;Cross-references: EMBL:X14098

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>

F:15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>

F:15-108/Domain: V region (V-kappa-1) <VRE>

F:30-103/Domain: immunoglobulin homology <IMM>

F:109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 88.2%; Score 492; DB 2; Length 132;
 Best Local Similarity 86.1%; Pred. No. 4.3e-33;
 Matches 93; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPAR 60
 Db 15 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPAR 74

Qy 61 FSGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA 108
 Db 75 FSGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKRA 122

RESULT 4

PC4405

Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 21-Jan-2000

C;Accession: PC4405

R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.

Chinese Biochem. J. 12, 648-653, 1996

A;Title: Generation of a phage display library of the immunoglobulin repertoire from human

A;Reference number: PC4405

A;Accession: PC4405
 A;Molecule type: mRNA
 A;Residues: 1-107 <DEN>
 A;Experimental source: spleen cell
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.3%; Score 487; DB 2; Length 107;
 Best Local Similarity 87.9%; Pred. No. 8.9e-33;
 Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPAR 60
 Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPAR 60

Qy 61 FSGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKR 107
 Db 61 FSGSGSGTSYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKR 107

RESULT 5

D38601

Ig kappa chain V region (6A7) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000

C;Accession: D38601

R;Goshorn, S.C.; Retzel, E.; Jermerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same anti

A;Reference number: A38601; MUID:91115823; PMID:1703527

A;Accession: D38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-99 <GOS>

A;Cross-references: GB:M57981; NID:gl96408; PIDN:AAA63362.1; PID:gl96409

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 486; DB 2; Length 99;
 Best Local Similarity 94.9%; Pred. No. 1e-32;
 Matches 94; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 9 AIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPARFSGSGGT 68
 Db 1 AIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTSLASGVPARFSGSGGT 60

Qy 69 SYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKR 107
 Db 61 SYSLTISRMEADAATYCCQORSSYPFTFGSGTKLEIKR 99

RESULT 6

A32513

Ig kappa chain precursor V region (MRL22) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C;Accession: A32513

R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization a

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: A32513

A;Molecule type: DNA

A;Residues: 1-130 <KOF>

A;Cross-references: GB:M20834; NID:gl96943; PIDN:AAA38846.1; PID:gl96944

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 483; DB 2; Length 130;
 Best Local Similarity 87.9%; Pred. No. 2.2e-32;
 Matches 94; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

RESULT 9

A: Gene: V(Kappa)Ox1
C: Incons: 17/1
C: Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
F: I-22/Domain: signal sequence #status predicted <SIG>

F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide bonds: #status predicted

Query Match 84.8%; Score 473; DB 1; Length 130;
Best Local Similarity 86.9%; Pred. No. 1.4e-31;
Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 61
Db 24 IVLTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 83
Qy 62 SGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIKRA 108
Db 84 SGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIKRA 130

RESULT 11

PS0070
Ig kappa chain V region (38C13.V6.1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0070
J. Levy, S.; Campbell, M.J.; Levy, R.
R. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0070
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 472; DB 2; Length 106;
Best Local Similarity 83.0%; Pred. No. 1.4e-31;
Matches 88; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPAR 60
Db 1 EIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPAR 60
Qy 61 FSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 106
Db 61 FSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 106

RESULT 12

S26338
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26338
R. Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26338
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-105 <STA>
A:Cross-references: EMBL:X59197; NID:952328; PIDN:CAAA1907.1; PID:g1334069
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 470; DB 2; Length 105;
Best Local Similarity 88.5%; Pred. No. 2.1e-31;
Matches 92; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 61
Db 24 IVLTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 83

Db 2 IVLTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 61
Qy 62 SGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEI 105
Db 62 SGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEI 105

RESULT 13

S66536
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66536
R. Tsiotis, G.; Haase, W.; Engel, A.; Michel, H.
Eur. J. Biochem. 231, 823-830, 1995
A:Title: Isolation and structural characterization of trimeric cyanobacterial photosy
A:Reference number: S66536; MUID:95377318; PMID:7649183
A:Accession: S66536
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <TST>
A:Cross-references: EMBL:X88903; NID:9895870; PIDN:CAA61365.1; PID:g1103702
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 466; DB 2; Length 120;
Best Local Similarity 83.5%; Pred. No. 4.9e-31;
Matches 91; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVP 58
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVP 60
Qy 59 ARFSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIKR 107
Db 61 ARFSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIKR 109

RESULT 14

S29591
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S29591
R. Kavalier, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S29591
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <KAV>
A:Cross-references: EMBL:X59094; NID:952227; PIDN:CAAA1820.1; PID:g52228
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 465; DB 2; Length 103;
Best Local Similarity 88.3%; Pred. No. 5.1e-31;
Matches 91; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 61
Db 1 IVLTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIYSTNSLASGVPARF 60
Qy 62 SGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLE 104
Db 61 SGSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLE 103

RESULT 15

PD0011
Ig kappa chain V region (VLB10, anti-AFP) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000
 C:Accession: PD0011
 R:Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
 Chinese Biochem. J. 12, 648-653, 1996
 A:Title: Generation of a phage display library of the immunoglobulin repertoire from hum
 A:Reference number: PC4405
 A:Contents: Spleen
 A:Accession: PD0011
 A:Molecule type: mRNA
 A:Residues: 1-107 <DEN>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 465; DB 2; Length 107;
 Best Local Similarity 85.0%; Pred No. 5.3e-31;
 Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTSNLASCVPAR 60
 Db 1 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTSNLASCVPAR 60
 QY 61 FSGSGSGTSYSLTISRVEAEDAATYCCQWRDNPPTPGGKLEIKR 107
 Db 61 FSGSGSGTSYSLTISRVEAEDAATYCCQWRDNPPTPGGKLEIKR 107

Search completed: December 23, 2002, 07:31:38
 Job time : 21.3488 secs

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DR EMBL; K00739; AAA38684.1; -.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Hybridoma.

FT DOMAIN 1 23

FT DOMAIN 24 33 FRAMEWORK-1.

FT DOMAIN 34 48 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 49 55 FRAMEWORK-2.

FT DOMAIN 56 87 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 58 96 FRAMEWORK-3.

FT DOMAIN 88 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 97 106 FRAMEWORK-4.

FT DISULFID 23 87

FT NON_TER 107 107 BY SIMILARITY.

SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECB550 CRC64;

Query Match 81.7%; Score 456; DB 1; Length 107;

Best Local Similarity 83.0%; Pred. No. 6.9e-39;

Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSAGVPAF 61

Db 2 IVLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSAGVPAF 61

QY 62 SGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107

Db 62 SGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107

RESULT 5

KV6G_MOUSE

ID KV6G_MOUSE STANDARD; PRT; 107 AA.

AC P04941;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-VI region NQ2-48.2.2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-

RT phenylloxazalone and its early diversification.";

RL Nature 304:320-324(1983).

CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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DR EMBL; K00737; AAA38682.1; -.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Hybridoma.

FT DOMAIN 1 23

FT DOMAIN 24 33 FRAMEWORK-1.

FT DOMAIN 34 48 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 49 55 FRAMEWORK-2.

FT DOMAIN 56 87 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 58 96 FRAMEWORK-3.

FT DOMAIN 88 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 97 106 FRAMEWORK-4.

FT DISULFID 23 87

FT NON_TER 107 107 BY SIMILARITY.

SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 81.5%; Score 455; DB 1; Length 107;

Best Local Similarity 83.0%; Pred. No. 8.7e-39;

Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSAGVPAF 61

Db 2 ILLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSAGVPAF 61

QY 62 SGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107

Db 62 SGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107

RESULT 6

KV6G_MOUSE

ID KV6G_MOUSE STANDARD; PRT; 108 AA.

AC P04945;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-VI region NQ2-6.1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-

RT phenylloxazalone and its early diversification.";

RL Nature 304:320-324(1983).

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DR EMBL; K00746; AAA38691.1; -.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Hybridoma.

FT DOMAIN 1 23

FT DOMAIN 24 33 FRAMEWORK-1.

FT DOMAIN 34 48 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 49 55 FRAMEWORK-2.

FT DOMAIN 56 87 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 88 98 FRAMEWORK-3.

FT DOMAIN 99 108 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 23 87

FT NON_TER 108 108 BY SIMILARITY.

SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match 80.6%; Score 450; DB 1; Length 108;

Best Local Similarity 82.2%; Pred. No. 2.8e-38;

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Matches 88% Conservative 10; Mismatches 7; Indels 2; Gaps 1;
QY 2 IELTQSPALMSAPGKVTITCSASSSVSYMHVFOQKPGTSPKLIWYSTNLSAGVPAVF 61
Db 2 IELTQSPALMSAPGKVTITCSASSSVSYMHVFOQKPGTSPKLIWYSTNLSAGVPAVF 61
QY 62 SCGSGTSTSLTISRMEDAAATYCCQSSYP--FTFGSGTKLEIKR 106
Db 62 SCGSGTSTSLTISRMEDAAATYCCQSSYP--FTFGSGTKLEIKR 108

RESULT 7
KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR PIR: A01941; KVMX4.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11584 MW; 366D022A5EC34D7 CRC64;

Query Match 77.6%; Score 433; DB 1; Length 107;
Best Local Similarity 82.4%; Pred. No. 1.4e-36;
Matches 89; Conservative 5; Mismatches 12; Indels 2; Gaps 2;
QY 1 DIELTQSPALMSAPGKVTITCSASSSVSYMHVFOQKPGTSPKLIWYSTNLSAGVPAVF 60
Db 1 DIELTQSPALMSAPGKVTITCSASSSVSYMHVFOQKPGTSPKLIWYSTNLSAGVPAVF 60
QY 61 FSGSGTSTSLTISRMEDAAATYCCQSSYP--FTFGSGTKLEIKR 107
Db 61 FSGSGTSTSLTISRMEDAAATYCCQ--WNYPLTFGGTKLEIKR 107

RESULT 8
KV6A_MOUSE
ID KV6A_MOUSE STANDARD; PRT; 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR PIR: A01941; KVMX4.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;

Query Match 77.1%; Score 430; DB 1; Length 107;
Best Local Similarity 81.5%; Pred. No. 2.7e-36;
Matches 88; Conservative 6; Mismatches 12; Indels 2; Gaps 2;
QY 1 DIELTQSPALMSAPGKVTITCSASSSVSYMHVFOQKPGTSPKLIWYSTNLSAGVPAVF 60
Db 1 EIVLTQSPALMSAPGKVTITCSASSSVSYMHVFOQKPGTSPKLIWYSTNLSAGVPAVF 60
QY 61 FSGSGTSTSLTISRMEDAAATYCCQSSYP--FTFGSGTKLEIKR 107
Db 61 FSGSGTSTSLTISRMEDAAATYCCQ--WNYPLTFGGTKLEIKR 107

RESULT 9
KV6D_MOUSE
ID KV6D_MOUSE STANDARD; PRT; 107 AA.
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region SAPC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR PIR: A01941; KVMX4.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;
```



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FT DOMAIN      49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN      56 87 FRAMEWORK-3.
FT DOMAIN      88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN      97 106 FRAMEWORK-4.
FT DISULFID    23 87 BY SIMILARITY.
FT NON_TER    107 107
SQ SEQUENCE    107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match      76.9%; Score 429; DB 1; Length 107;
Best Local Similarity 81.5%; Pred. No. 3.4e-36;
Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 1 DIELTQSPALMSAPGKVTITCSASSSVSMHWFOQKPGTSPKLTWYSTNLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPALTAASLGKVTITCSASSSVSMHWYQKSGTSPKPIYIEISKLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYP-FTFGSGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 FSGSGGTSYSLTISRMEADAATYYCQQ-WNYPLITFGGAGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match      76.9%; Score 429; DB 1; Length 107;
Best Local Similarity 81.5%; Pred. No. 3.4e-36;
Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 1 DIELTQSPALMSAPGKVTITCSASSSVSMHWFOQKPGTSPKLTWYSTNLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPALTAASLGKVTITCSASSSVSMHWYQKSGTSPKPIYIEISKLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYP-FTFGSGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 FSGSGGTSYSLTISRMEADAATYYCQQ-WNYPLITFGGAGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match      76.7%; Score 428; DB 1; Length 107;
Best Local Similarity 80.6%; Pred. No. 4.3e-36;
Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPALMSAPGKVTITCSASSSVSMHWFOQKPGTSPKLTWYSTNLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

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Db 1 EIVLTQSPALTAASLGKVTITCSASSSVSMHWYQKSGTSPKPIYIEISKLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYP-FTFGSGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 FSGSGGTSYSLTISRMEADAATYYCQQ-WNYPLITFGGAGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match      76.9%; Score 429; DB 1; Length 107;
Best Local Similarity 81.5%; Pred. No. 3.4e-36;
Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 1 DIELTQSPALMSAPGKVTITCSASSSVSMHWFOQKPGTSPKLTWYSTNLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPALTAASLGKVTITCSASSSVSMHWYQKSGTSPKPIYIEISKLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYP-FTFGSGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 FSGSGGTSYSLTISRMEADAATYYCQQ-WNYPLITFGGAGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match      76.7%; Score 428; DB 1; Length 107;
Best Local Similarity 80.6%; Pred. No. 4.3e-36;
Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPALMSAPGKVTITCSASSSVSMHWFOQKPGTSPKLTWYSTNLASGVPAR 60
   :|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

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DB 26 LTQSPALMAASLGQVMTWCSSSVSSSYLHWYQKSGSPKPLTHRTSNLASGVPARF 8
QY 62 SGGSGTSYSLTISMEAEADAATYTCOORSYPTFTGSGTKLEIKR 107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 86 SGGSGTSYSLTISSEAEADAATYTCOOWSGYP--FGSGTKLEIKR 129
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RA "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RL PIR; A01937; KMS43.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 66.9%; Score 373.5; DB 1; Length 111;
Best Local Similarity 65.8%; Pred. No. 1.2e-30;
Matches 73; Conservative 13; Mismatches 20; Indels 5; Gaps

QY 1 DIELTQSPALMASPGEKVITTCASSSV-----SYWHWFQKPGTSPKLWITSYNLAS 55
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 DVLVLTQSPALAVSLGQRATISCKASQSDVDGDSYNNYQKPGPPKPLLIYAASNL 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 56 GVPARFSGSGTSTYSLTISMEAEADAATYTCOORSYPTFTGSGTKLEIK 106
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 GIPARFSGSGTDTFLNIHPVEEADAATYTCQSNEDFTFGSGTKLEIK 111
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
KV1V_HUMAN
ID KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;

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RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; K1HJEN.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 66.0%; Score 368.5; DB 1; Length 108;
Best Local Similarity 64.8%; Pred. No. 3.7e-30;
Matches 70; Conservative 17; Mismatches 20; Indels 1; Gaps 1;

QY 1 DIETQSPAIMSASPGKVTITCSASSV-SYMHWFQKPGTSPKLIYSTSNLASG 59
Db 1 DIQLTQSPSSLSASVGDRTTICRASQSYNYVAFQKPGKAPKSLIYDASTLQSGVPS 60

QY 60 RFSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
Db 61 NFTGSGSGDTFILTISLQPEPATYYCQYNSYPYTFGQGTQVQIKR 108

RESULT 15
KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 66.0%; Score 368.5; DB 1; Length 111;
Best Local Similarity 64.9%; Pred. No. 3.8e-30;
Matches 72; Conservative 14; Mismatches 20; Indels 5; Gaps 1;
```

```
QY 1 DIETQSPAIMSASPGKVTITCSASSV-----SYMHWFQKPGTSPKLIYSTSNLAS 55
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYMNWYQKPGQPPKLLIYTASNLES 60

QY 56 GVPAREFSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 GIPAREFSGSGTDFTLNIHPVEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
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Search completed: December 23, 2002, 07:26:11
Job time : 10.6744 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 44.7907 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-8

Perfect score: 558

Sequence: 1 DIETQSPAIMSASPGKVT.....QRSSYPFTGSGTKLEIKRA 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_prodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	90.0	134	11 Q8VDD0	Q8vdd0 mus musculo
2	470	84.2	106	5 Q90410	Q90410 schistosoma
3	442	79.2	235	11 Q91W12	Q91w12 mus musculo
4	434.5	77.9	97	11 Q91L76	Q91l76 mus musculo
5	403.5	72.3	101	11 Q91L78	Q91l78 mus musculo
6	380.5	68.2	234	11 Q8R062	Q8r062 mus musculo
7	371.5	66.6	214	11 Q9R1A5	Q9r1a5 mus musculo
8	365.5	65.5	108	4 Q90L77	Q90l77 homo sapien
9	365.5	65.5	111	11 Q920E9	Q920e9 mus musculo
10	361	64.7	107	4 Q96SA9	Q96sa9 homo sapien
11	361	64.7	109	4 Q9UL78	Q9ul78 homo sapien
12	359.5	64.4	108	4 Q9UL70	Q9ul70 homo sapien
13	357.5	64.1	108	4 Q90L79	Q90l79 homo sapien
14	356.5	63.9	234	11 Q91WF8	Q91wf8 mus musculo
15	356.5	63.9	234	11 Q8VCP0	Q8vcp0 mus musculo
16	354.5	63.5	233	11 Q91WS9	Q91ws9 mus musculo

17	353	63.3	107	4	Q9UL81	Q9ul81 homo sapien
18	351.5	63.0	298	11	Q9QYF0	Q9qyf0 mus musculo
19	347.5	62.3	109	11	Q920E6	Q920e6 mus musculo
20	346.5	62.1	108	4	Q9UL83	Q9ul83 homo sapien
21	342.5	61.4	107	11	Q9JL84	Q9jl84 mus musculo
22	342	61.3	109	4	Q9UL86	Q9ul86 homo sapien
23	337.5	60.5	108	11	Q8VIJ0	Q8vij0 mus musculo
24	337	60.4	109	4	Q9UL85	Q9ul85 homo sapien
25	331	59.3	238	11	Q99M37	Q99m37 mus musculo
26	323	57.9	238	11	Q8VC16	Q8vc16 mus musculo
27	321.5	57.6	127	11	Q925S9	Q925s9 mus musculo
28	320.5	57.4	116	4	Q96PF6	Q96pf6 homo sapien
29	313	56.1	239	11	Q8VC55	Q8vc55 mus musculo
30	308.5	55.3	103	11	Q9JL80	Q9jl80 mus musculo
31	307	55.0	239	4	Q8TCD0	Q8tcd0 homo sapien
32	300.5	53.9	107	11	Q9ER29	Q9er29 mus musculo
33	297	53.2	104	11	Q9JL82	Q9jl82 mus musculo
34	295.5	53.0	114	4	Q9UL80	Q9ul80 homo sapien
35	295	52.9	241	11	Q921A6	Q921a6 mus musculo
36	292.5	52.4	99	11	Q9JL74	Q9jl74 mus musculo
37	286.5	51.3	234	11	Q8R028	Q8r028 mus musculo
38	281	50.4	237	4	Q8WTU6	Q8wtu6 homo sapien
39	276	49.5	237	4	Q8WUK4	Q8wuk4 homo sapien
40	260.5	46.7	109	6	Q9N0W5	Q9n0w5 oryctolagus
41	259	46.4	233	4	Q8TBC9	Q8tbc9 homo sapien
42	247.5	44.4	236	4	Q96E61	Q96e61 homo sapien
43	244	43.7	107	4	Q9NSD6	Q9nsd6 homo sapien
44	244	43.7	110	4	Q8TE63	Q8te63 homo sapien
45	243	43.5	108	4	Q96SB0	Q96sb0 homo sapien

ALIGNMENTS

RESULT 1

Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Anti-MOG 212 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chernajovsky Y.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Semi P.;
RT "Targeting T cells to the CNS";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CDFP8E2236E2D0CF CRC64;

Query Match 90.0%; Score 502; DB 11; Length 134;
Best Local Similarity 89.7%; Pred. No. 3.8e-45;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSMHWFQKPGTSPKLWIYSTSNLASGVPARF 61

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Db 24 IVLTQSPAIMSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARF 83
Qy 62 SSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIKRA 108
Db 84 SSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIKRA 130

RESULT 2
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum".
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 84.2%; Score 470; DB 5; Length 106;
Best Local Similarity 87.4%; Pred. No. 6.5e-42;
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARFSG 63
Db 4 LTQSPAIMSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARFSG 63

Qy 64 SSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 106
Db 64 SSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 106

RESULT 3
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Unknown (protein for WGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
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Query Match 79.2%; Score 442; DB 11; Length 235;
Best Local Similarity 81.3%; Pred. No. 1.5e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARF 61
Db 24 IVLTQSPAIMSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARF 83

Qy 62 SSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIKRA 108
Db 84 SSGSGTSYSLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIKRA 130

RESULT 4
Q9JL76
ID Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin".
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9E1FFE1F49DA1C CRC64;

Query Match 77.9%; Score 434.5; DB 11; Length 97;
Best Local Similarity 86.6%; Pred. No. 3.1e-38;
Matches 84; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Qy 11 MSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARFSGSGTSY 70
Db 1 LSASPGKVTITCSASSSYMHWFQKPGTSPKRWIYDTSKLASGVPARFSGSGTSY 60

Qy 71 SLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 106
Db 61 SLTISRMEADAATYYCQQRSSYPPTFGSGTKLEIK 97

RESULT 5
Q9JL78
ID Q9JL78 PRELIMINARY; PRT; 101 AA.
AC Q9JL78;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)".
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF152371; RAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_llike; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER      1
FT              214    214
FT FT            1
FT NON_TER      108   108
FT FT            1
FT NON_TER     108   108
SQ SEQUENCE      214 AA; 23922 MW; 52BA205FEDE995E2A CRC64;

Query Match          66.6%; Score 371.5; DB 11; Length 214;
Best Local Similarity 67.0%; Pred.No. 3.3e-31;
Matches       73; Conservative           9; Mismatches 26; Indels   1; Gaps   1;

QY      1 DIELTQSPTAMASPGKVTITCSASSV-SYMHWFOOKPGCTSPKLWIYSNLSAGVPA 59
Db             ||||| | | | | | | | | : ||: ||||||| | | : | |||:
               1 DIQLTQSPSSMYASLGSRVITCKASODINSYLSWFQQKGPKSKTLIYRANRLVDGVP 60
QY      60 RFSGGGSTGYSLTIISMEADAATYTCQORSSYPFTFGSGTKLEIKRA 108
Db             ||||| | | | | | | | | | | -:||| | | | | | | | | |
               61 RFSGGGGQGYSLTFISSLEYEDMGIIYCLQYDEFPPFTFGSGTKLEIKRA 109


RESULT 8
Q9UL77 PRELIMINARY; PRG; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DD 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT DT 01-DIC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiade; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;.
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RY Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR DR SMART; SM00410; IG_llike; 1.
FT NON_TER      1
FT              108   108
FT FT            1
FT NON_TER     108   108
SQ SEQUENCE     108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match          65.5%; Score 365.5; DB 4; Length 108;
Best Local Similarity 63.9%; Pred.No. 6.3e-31;
Matches       69; Conservative        20; Mismatches 18; Indels   1; Gaps   1;

QY      1 DIELTQSPTAMASPGKVTITCSASSV-SYMHWFOOKPGCTSPKLWIYSNLSAGVPA 59
```

Db	1	DIQMTQSPSSLSASVDGRVTITCRASQISISLYLNWYQOKPGKAPNLLIIAASLSQGPS	60
Qy	60	RFGSGSGTSLTISRMEADATYYCQQRSSYPPTFGSGTKLEKR	107
Db	61	RFGSGSGTDTLTSSLPEDFATYYCQOSYSTSWTFEGTKVEIKR	108

RESULT 9
Q920E9
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE pterin-mimicking anti-idiotypic kappa chain variable region

OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RA	Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;	
RT	"Definition of the Idiotype of Pterin-Mimicking Antibodies Expressed	
RT	in Mammalian Cells.";	
RT	Submitted (SEP-2000) to the EMBL/GenBank/DBSJ databases.	
DR	EMBL; AF307935; AAL09419.1; -	
DR	InterPro; IPR003006; Ig_MHC.	
DR	Pfam; PF00047; Ig; 1.	
FT	NON_TER 1	
FT	NON_TER 111	
FT	NON_TER 111	
FT	SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;	

Query Match	65.5%	Score 365.5	DB 11	Length 111
Best Local Similarity	64.9%	Pred. No. 6.5e-31		
Matches 72	Conservative 10	Mismatches 24	Indels 5	Gaps 1

Qy	1	DIELQSPAINASPEGEKVITCSASSV-----SYMHWFQOKPQKTSFKLWITYSTSNLAS	55
Db	1	DIIVLTQSPASLSLQGRATISCRASKSVTSYGYIMHWYQOKPQKPPKLLIYASNLDS	60
Qy	56	GYPARFSGSGSGTYSLTISRMEADDAATYVQCQRSSYPFTFGSGTKLEIK	106
Db	61	GYPARFSGSGSGTFTLIHNPVEEDAAATYVQHSRELDPYFEGGQTKLEIK	111

RESULT 10
Q96SA9
ID Q96SA9
PRELIMINARY:
PRT: 107 AA.

AC	Q95A93	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)	
DE	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain	
DE	variable region (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

KN	SEQUENCE FROM N.A.	
RP	MEDLINE=98375893; PubMed=9712075;	
RA	Addresson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;	
RR	"Molecular analysis of polyreactive monoclonal antibodies from	
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin	
RT	antibody V region genes";	
RL	J. Immunol. 161:2020-2031(1998).	
RL	EMBL: U96396; AAB68785.1; -.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	Pfam: PF00047; Ig; 1.	
DR	NON_TER 1	1
FT	NON_TER 107	107

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SQ  SEQUENCE  107 AA;  11520 MW;  4BB43E9C5B577F16  CRC64;

Query Match      64.7%;  Score 361;  DB 4;  Length 107;
Best Local Similarity  64.8%;  Pred. No. 1.8e-30;
Matches 70;  Conservative 19;  Mismatches 17;  Indels 2;  Gaps

Qy  1  DIETQSPAINASPGKEVTTITCSASSSV-SYMHWFQOKPGTSPKLTWYSTNSLASGVPA 59
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  1  DIQWTQSPSSLSASVGDVTTITCRASQISSYLWNYQOKPGKAPKLLIYASSSLQSGVPS 60

Qy  60  RFGSGSGGTYSYSLTISRMAEDAAITYCQQRSSYPFTFGSGTKLEIKR 107
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  61  RFSGSGSGGTDFYTISSILOPEDFATYTCOOSYS-TIFEGGKTKVEIKR 107
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

RESULT 11
Q9UL78
ID Q9UL78
PRELIMINARY: PRT: 109 AA.

AC Q30L78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 111

RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; Pubmed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RA	"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RT	Clin. Immunol. Immunopathol. 87:184-192(1998).
RL	ENBL; AF035036; AAD56272.1; -.
DR	HSSP; P80362; 1WTL.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_v.
DR	Pfam; PF00047; ig.1
DR	SMART; SM00406; IGV; 1.
FT	NON_TER 1
FT	NON_TER 109
FT	NON_TER 109
SO	SEQUENCE 109 AA; 5FG75C52EC7BE197 CRC64;

Query Match 64.7%; Score 361; DB 4; Length 109;
Best Local Similarity 62.4%; Pred. No. 1.9e-30;
Matches 68; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

Qy	1	DIETQSPATMSAPGKPVITCSASSV--SYMHWFQKPGTSPKLIWYVSTSNL	AGVP	58
Db	1	EIVTQPGTSLSPGPRATLSRASVS	SSYLAWYQKPGQAPRLLIYGASSRATGIP	60
Qy	59	ARFSGSGGTSYSLITSRMEADAA	TYCYQQRSSYPFFSGTGLEIKR	107
Db	61	DRFSGSGGTDFTLTISRLEPEDCA	VYCYCOYGGSPITFGGTKEIKR	109

RESULT 12
Q9UL70
ID Q9UL70
PRELIMINARY:
PRT: 108 AA:

AC	Q30LR0;
AD	01-MAY-2000 (TReMBLrel. 13, Created)
AE	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
AF	01-DEC-2001 (TReMBLrel. 19, Last annotation update)
AG	01-DRC-2001 (TReMBLrel. 19, Last annotation update)
AH	Myosin-reactive immunoglobulin light chain variable region
AI	(Fragment).
AL	Homo sapiens (Human).
AM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AN	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AO	NCBI_TaxID=9606;
AP	[1]


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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT 108
FT SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match 64.4%; Score 359.5; DB 4; Length 108;
Best Local Similarity 63.9%; Pred. No. 2.7e-30;
Matches 69; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

QY 1 DIETQSPAIMSASPGKVTITCSASSVS-YMHWFQOKPGTSPKLIYSTSNLASGVPA 59
Db 1 DIQMTPSSLSASVGDRTVITCRASQGISNYLAWYQQKPKVPSLIYAASTLQSGVPS 60
QY 60 RFGSGSGTYSILTISRMEADAATYCCOQRSSYPFTFGSGTKLEIKR 107
Db 61 RFGSGSGTDFTLTISLQPEDVAITYCQKYNAPFTFGSGTKLEIKR 108

RESULT 13
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; RAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT 108
FT SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 64.1%; Score 357.5; DB 4; Length 108;
Best Local Similarity 62.0%; Pred. No. 4.4e-30;
Matches 67; Conservative 21; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIETQSPAIMSASPGKVTITCSASSV-YMHWFQOKPGTSPKLIYSTSNLASGVPA 59
Db 1 DIVMTQSPSLASTGDRVTISCRMSQGISNYLAWYQQKPKRAPELLIYAASTLQSGVPS 60
QY 60 RFGSGSGTYSILTISRMEADAATYCCOQRSSYPFTFGSGTKLEIKR 107
Db 61 RFGSGSGTDFTLTISLQSEDAITYCQYVFPFTFGQGTKEIKR 108
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RESULT 14
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB781D2D CRC64;

Query Match 63.9%; Score 356.5; DB 11; Length 234;
Best Local Similarity 63.3%; Pred. No. 1.4e-29;
Matches 69; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 DIETQSPAIMSASPGKVTITCSASSVS-YMHWFQOKPGTSPKLIYSTSNLASGVPA 59
Db 21 DIQMTPSSLSASLGDRTVITCRASQDISNYLWYQQKPDGTVKLLIYTSRLYLGVS 80
QY 60 RFGSGSGTYSILTISRMEADAATYCCOQRSSYPFTFGSGTKLEIKR 108
Db 81 RFGSGSGTYSILTISNLQEDATYFCQGNTPPTFGSGTKLEVKA 129

RESULT 15
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 63.9%; Score 356.5; DB 11; Length 234;
Best Local Similarity 63.3%; Pred. No. 1.4e-29;
Matches 69; Conservative 15; Mismatches 24; Indels 1; Gaps 1;
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 : Search time 9.12597 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-21

Perfect score: 101

Sequence: 1 WIDPENGSDYAPKFGQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	17	AAE13138	Humanised antibody
2	101	100.0	17	AAE13138	VEGF antagonist an
3	101	100.0	17	AAE13138	Heavy chain comple
4	101	100.0	117	AAE13143	Humanised antibody
5	101	100.0	117	AAE13143	VEGF antagonist an
6	101	100.0	117	AAE13143	Antigen-binding pr
7	101	100.0	136	AAE13145	Chimeric picil hea
8	101	100.0	136	AAE13145	VEGF antagonist an
9	101	100.0	238	AAE13145	Antigen-binding pr
10	94	93.1	17	AAE13138	Anti-p53 monoclon

11	94	93.1	17	21	AAE13138	Complementary dete
12	94	93.1	17	23	AAE13138	Heavy chain comple
13	94	93.1	20	21	AAE13138	Murine anti-p53 PA
14	94	93.1	112	20	AAE13138	Anti-p53 monoclon
15	94	93.1	116	21	AAE13138	Murine anti-p53 mo
16	94	93.1	117	21	AAE13138	Variable heavy cha
17	94	93.1	117	23	AAE13138	Antigen-binding pr
18	94	93.1	122	20	AAE13138	Humanised Murine C
19	94	93.1	124	15	AAE13138	Anti-carcinoembryo
20	94	93.1	124	15	AAE13138	Anti-carcinoembryo
21	94	93.1	124	15	AAE13138	Murine COL1 VH cha
22	94	93.1	124	20	AAE13138	Humanised Murine C
23	94	93.1	124	20	AAE13138	Humanised Murine C
24	94	93.1	124	20	AAE13138	Humanised Murine C
25	94	93.1	124	20	AAE13138	Humanised Murine C
26	94	93.1	124	20	AAE13138	Humanised Murine C
27	94	93.1	124	20	AAE13138	Humanised Murine C
28	94	93.1	124	20	AAE13138	Humanised Murine C
29	94	93.1	124	20	AAE13138	Humanised Murine C
30	94	93.1	124	20	AAE13138	Humanised Murine C
31	94	93.1	124	23	AAE13138	Murine Col-1(CEA a
32	94	93.1	124	23	AAE13138	Humanised COL-1(CE
33	94	93.1	124	23	AAE13138	Humanised COL-1(CE
34	94	93.1	124	23	AAE13138	Humanised COL-1(CE
35	94	93.1	124	23	AAE13138	Humanised COL-1(CE
36	94	93.1	124	23	AAE13138	Humanised COL-1(CE
37	94	93.1	124	23	AAE13138	Humanised COL-1(CE
38	94	93.1	124	23	AAE13138	Humanised COL-1(CE
39	94	93.1	124	23	AAE13138	Humanised COL-1(CE
40	94	93.1	124	23	AAE13138	Humanised COL-1(CE
41	94	93.1	124	23	AAE13138	Humanised COL-1(CE
42	94	93.1	124	23	AAE13138	Humanised COL-1(CE
43	94	93.1	240	23	AAE13138	Protein template u
44	94	93.1	243	19	AAE13138	Antigen-binding pr
45	94	93.1	270	16	AAE13138	Single chain antib
						MFE-23 antibody.

ALIGNMENTS

RESULT 1
AAE13138
ID AAE13138 standard; peptide: 17 AA.
AC AAE13138;
XX
XX 28-JAN-2002 (first entry)
DF
XX Humanised antibody murine heavy chain hypervariable region (VH) CDR2.

DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
XX cytosstatic; heavy chain hypervariable region; VH; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
OS
XX Mus sp.
XX
XX WO200174296-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10504.
XX
XX 31-MAR-2000; 2000US-0540770.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (CORR) CORNELL RES FOUND INC.
XX
XX Witte L, Rafii S;
XX
XX WPI; 2001-662942/76.
XX
XX N-PSDB; AAD21664.

PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -

XX Claim 8; Page 14; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid
CC tumor cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody murine heavy chain hypervariable region (VH) CDR-2 used in the
CC exemplification of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 101; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.4e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17

Db 1 WIDPENGSDYAPKFOG 17

RESULT 2

AAB82704

ID AAB82704; standard; Peptide; 17 AA.

XX AAB82704

XX AAB82704

XX AAB82704

DT 15-OCT-2001 (first entry)

DE VEGF antagonist antibody IMC-1C11 VH CDR-2.

XX IMC-1C11: chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumor; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumor; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
KW complementarity determining region.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

OS WO20015723-A1.

PN 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US02839.

XX 28-JAN-2000; 2000US-0178791.

XX 31-MAR-2000; 2000US-0539692.

XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Kerbel R;

XX WPI; 2001-514531/56.

XX Treating or controlling an angiogenic dependent condition (e.g. a

XX neoplasm, collagen-vascular or autoimmune disease) in mammal by

XX administering a combination of an antiangiogenic molecule and a

XX chemotherapeutic agent

XX Disclosure; Page 37; 42pp; English.

XX The present sequence is that of complementarity determining region
CC 2 of the heavy chain variable region (see also AAB82701) of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.

CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX Sequence 17 AA;

Query Match 100.0%; Score 101; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.4e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17

Db 1 WIDPENGSDYAPKFOG 17

RESULT 3

AAU74416

ID AAU74416 standard; peptide; 17 AA.

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

XX AAU74416;

CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (C1 domain), and P2 has an antigen-binding
CC site located to the N terminus of the C1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the heavy chain variable domain
CC complementarity determining region H2 (CDRH2) version #2 incorporated
CC into an antigen-binding protein described in the method of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 101; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 1 WIDPENGSDYAPKFG 17
|||||

RESULT 4

AAE13143
ID AAE13143 standard; Protein; 117 AA.

AC AAE13143;

XX 28-JAN-2002 (first entry)

DE Humanised antibody heavy chain fragment.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cystostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX WO200174296-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.

DR N-PSDB; AAD21669.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -

XX Claim 8; Page 15; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain fragment used in the exemplification of the
CC invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 101; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
Db 50 WIDPENGSDYAPKFG 66
|||||

RESULT 5

AA82709
ID AA82709 standard; Protein; 117 AA.

XX AA82709;

XX 15-OCT-2001 (first entry)

DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.

XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers
FT Region 26..35
FT /label= CDR-H1
FT /note= "complementarity determining region 1"

FT Region 50..66
FT /label= CDR-H2

FT /note= "complementarity determining region 2"

FT Region 99..106
FT /label= CDR-H3

FT /note= "complementarity determining region 3"

XX WO200154723-A1.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US02839.

XX 28-JAN-2000; 2000US-0178791.

XX 31-MAR-2000; 2000US-0539692.

XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.

XX Kerbel R;

XX WPI; 2001-514531/56.

DR N-PSDB; AAH26405.
 XX Treating or controlling an angiogenic dependent condition (e.g. a
 PT neoplasm; collagen-vascular or autoimmune disease) in mammal by
 PT administering a combination of an antiangiogenic molecule and a
 PT chemotherapeutic agent
 XX
 PS Disclosure; Page 38; 42pp; English.
 XX
 CC The present sequence is that of the heavy chain variable region of
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,
 CC or a fragment of it, can be used as an anti-angiogenic molecule,
 CC together with a chemotherapeutic agent, for the treatment of an
 CC angiogenic dependent condition in a mammal, especially a human.
 CC The invention relates generally to a method of treating or
 CC controlling an angiogenic dependent condition by administering an
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
 CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The antiangiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFGQ 17
 ||| ||||| ||||| |||||
 Db 50 WIDPENGSDYAPKFGQ 66

RESULT 6
 AAU74417
 ID AAU74417 standard; peptide; 117 AA.
 XX
 AC AAU74417;
 XX
 DT 26-MAR-2002 (first entry)
 XX

XX Antigen-binding protein heavy chain variable domain (VH) #2.

XX Antigen-binding protein; antibody heavy chain variable domain;
 KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 KW cell proliferation inhibitor.

XX Mus sp.
 OS
 XX WO200190192-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 24-MAY-2001; 2001WO-US16924.
 XX
 PF
 XX 24-MAY-2000; 2000US-206749P.
 PR
 XX (IMC1) IMCLONE SYSTEMS INC.
 PA
 XX Zhu Z;

PI
 XX WPI; 2002-106189/14.
 DR N-PSDB; AAS20288.
 DR
 XX

PT New bispecific immunoglobulin-like antigen-binding protein for reducing

PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides
 XX
 PS Claim 61; Page 60; 64pp; English.
 XX
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an Ig molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This sequence represents a heavy chain variable domain (VH) incorporated
 CC into Fv, an engineered protein containing a heavy chain variable domain
 CC and a light chain variable domain in one polypeptide chain, described in
 CC the method of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFGQ 17
 ||| ||||| ||||| |||||
 Db 50 WIDPENGSDYAPKFGQ 66

RESULT 7
 AAEL13145
 ID AAEL13145 standard; Protein; 136 AA.
 XX
 AC AAEL13145;
 XX
 DT 28-JAN-2002 (first entry)
 XX

XX Chimeric p1C11 heavy chain fragment.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytosolic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
 KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
 KW human; p1C11 vector.

XX Chimeric - Homo sapiens.
 OS Chimeric - Unidentified.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Leader_peptide
 FT Protein 20..136
 FT /note= "Mature chimeric p1C11 heavy chain fragment"
 FT Region 45..54
 FT /label= CDR_H1
 FT Region 69..85
 FT /label= CDR_H2
 FT Misc-difference 84

FT /note= "Residue 'O' is present at this location in the
 FT sequence shown in fig-11 of the specification"
 FT Misc-difference 101
 FT /note= "Residue 'O' is present at this location in the
 FT sequence shown in fig-11 of the specification"
 FT

```

FT Region 119..125
XX /label= CDR_H3
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10504.
XX
XX 31-MAR-2000; 2000US-0540770.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR ) CORNELL RES FOUND INC.
XX
XX Witte L, Rafii S;
XX
XX WPI; 2001-662942/76.
DR N-PSDB; AAD21682.
XX
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
XX Example 3; Fig 11; 68pp; English.
XX
XX The invention relates to a method for inhibiting the growth of non-solid
CC tumor cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC pIC11 heavy chain fragment which is used for the construction of chimeric
CC pIC11 IgG expression vector. Chimeric pIC11 heavy chain contains cloned
CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
CC domain (CH).
XX
XX Sequence 136 AA;
XX
XX Query Match 100.0%; Score 101; DB 22; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 WIDPENGSDYAPKFGQ 17
XX | | | | | | | | | | | | | | | | | |
XX Db 69 WIDPENGSDYAPKFGQ 85
XX
XX RESULT 8
XX AAB82701
XX ID AAB82701 standard; Protein: 136 AA.
XX
XX AC AAB82701;
XX
XX DT 15-OCT-2001 (first entry)
XX
XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
XX vascular endothelial growth factor; angiogenesis; antiangiogenic;
XX antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
XX tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
XX colon carcinoma; ovarian carcinoma; neuroblastoma;
XX glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX

```

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FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..136
FT /label= Mature_protein
FT Region 45..54
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT Region 59..85
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT Region 118..125
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
XX WO200154723-A1.
XX
XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US02839.
XX
XX 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
XX (IMCL-) IMCLONE SYSTEMS INC.
PA
PA Kerbel R;
XX
XX WPI; 2001-514531/56.
DR N-PSDB; AAH26413.
XX
XX Treating or controlling an angiogenic dependent condition (e.g. a
XX neoplasm, collagen-vascular or autoimmune disease) in mammal by
XX administering a combination of an antiangiogenic molecule and a
XX chemotherapeutic agent -
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX The present sequence is that of the heavy chain variable region of
XX IMC-1C11, a mouse-human chimeric antibody that has vascular
XX endothelial growth factor (VEGF) antagonist activity. The antibody,
XX or a fragment of it, can be used as an anti-angiogenic molecule,
XX together with a chemotherapeutic acid, for the treatment of an
XX angiogenic dependent condition in a mammal, especially a human.
XX The invention relates generally to a method of treating or
XX controlling an angiogenic dependent condition by administering an
XX anti-angiogenic molecule and a chemotherapeutic agent, to produce a
XX regression or arrest of the condition while minimising or
XX preventing significant toxicity of the chemotherapeutic agent.
XX The anti-angiogenic molecule inhibits or blocks the action of a
XX vascular endothelium survival factor such as VEGF or its receptor,
XX and is especially IMC-1C11. Conditions that can be treated include
XX a neoplasm, a collagen-vascular disease or an autoimmune disease,
XX especially a solid tumour, including breast carcinoma, lung
XX carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
XX ovarian carcinoma, neuroblastoma, central nervous system tumour,
XX neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
XX Sequence 136 AA;
XX
XX Query Match 100.0%; Score 101; DB 22; Length 136;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 WIDPENGSDYAPKFGQ 17
XX | | | | | | | | | | | | | | | | | |
XX Db 69 WIDPENGSDYAPKFGQ 85
XX
XX RESULT 9
XX AAU74420
XX ID AAU74420 standard; Protein: 238 AA.

```

AAU74420;
26-MAR-2002 (first entry)
Antigen-binding protein, single chain variable fragment version #2.
Antigen-binding protein; single chain variable fragment; svFv; antigen;
cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
vascular endothelial growth factor receptor; VEGF;
cell proliferation inhibitor.
Mus sp.
Synthetic.
Key Location/Qualifiers
Region 1..117 /label= VH
/note= "Heavy chain variable domain. Specifically
claimed in claim 61"
Region 118..132 /label= Linker
/note= "15 amino acid linker joins the VH and VL
regions of the single chain variable fragment
protein. Encoded by AAS20285"
Region 133..238 /label= VL
/note= "Light chain variable domain. Specifically
claimed in claim 61"
WO200190192-A2.
29-NOV-2001.
24-MAY-2001; 2001WO-US16924.
24-MAY-2000; 2000US-206749P.
(IMCL-) IMCLONE SYSTEMS INC.
Zhu Z;
WPI; 2002-106189/14.
New bispecific immunoglobulin-like antigen-binding protein for reducing
tumour growth and for inhibiting angiogenesis, comprises a complex of
two polypeptides and two second polypeptides -
Claim 63; Page 62-63; 64pp; English.
The invention describes an antigen-binding protein (I) comprising a
complex of two polypeptides (P1) and two second polypeptides (P2) which
are stably associated in an immunoglobulin like complex. P1 has an
antigen-binding site located to the N terminus of immunoglobulin (Ig)
light chain constant domain (CL domain), and P2 has an antigen-binding
site located to the N terminus of the CH1 domain. (I) is useful for:
neutralising the activation of a vascular endothelial growth factor
(VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
reducing endothelial cell proliferation; inhibiting VEGF induced
migration of human leukaemia cells; blocking interaction of a protein and
its ligand; promoting interactions between immune cells and target cells;
and in vivo and in vitro for investigative, diagnostic or treatment
methods. The design of (I) provides for efficient production so that
substantially all of the antigen-binding proteins produced are assembled
in the desired configuration. (I) is bivalent and bispecific, homogeneous
and tetrameric form. The heavy chain constant domains which constitute
the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
antibody and which provide other antibody functions can be present. There
is no requirement for processing in vitro to obtain the complete product.
This is the amino acid sequence of a single chain variable fragment
(scFv), an engineered protein containing a variable light and variable
heavy domain on one polypeptide, described in the method of the
invention.

XX SQ Sequence 238 AA;
Query Match 100.0%; Score 101; DB 23; Length 238;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDSYAPKFOG 17
|||||
DB 50 WIDPENGSDSYAPKFOG 66
RESULT 10
AAW89162
ID AAW89162 standard; peptide; 17 AA.
XX AC AAW89162;
XX DT 25-MAR-1999 (first entry)
XX DE Anti-p53 monoclonal antibody 421 CDR2 heavy chain based peptide.
XX KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
XX KW immune response; tumour associated antigen; metastatic cancer.
XX OS Mus sp.
XX OS Synthetic.
XX PN WO9856416-A1.
XX PD 17-DEC-1998.
XX PF 09-JUN-1998; 98WO-IL00266.
XX PR 09-JUN-1997; 97IL-0121041.
XX PA (YEDA) YEDA RES & DEV CO LTD.
PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
PI Wolkowicz R;
XX WPI; 1999-070296/06.
PT Use of a monoclonal antibody to a tumour-associated antigen - to
PT induce anti-tumour immunity or elicit an increased immune response
PT to the antigen
XX Claim 7; Page 29; 47pp; English.
XX The present invention describes the use of an immunogen (A) to induce
XX anti-tumour immunity; to elicit an increased immune response to tumour
XX associated antigen (TAA) and/or to induce an immune response to mutant
XX or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
XX (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
XX (complementarity determining region) on the heavy or light chain of MAB
XX (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
XX variable (V) region of MAB in a gene delivery vehicle. The present
XX sequence represents a peptide based on CDR2 of the heavy chain of
XX anti-p53 MAB 421. Also described is a method for generating sequence-
XX specific, anti-DNA antibodies (Ab) by immunising a mammal with a MAB
XX directed to a domain containing a DNA-binding site of a DNA-binding
XX protein. (A) is used to treat a wide variety of primary and metastatic
XX cancers, particularly those where p53 is involved. Ab are used for
XX diagnosis (e.g. to determine critical sequences in animal or plant
XX breeding); to identify bacteria and other parasites; to determine
XX paratage; in forensic science; to isolate specific genes for DNA
XX vaccination; in gene sequencing and cloning; also possibly for activation
XX of selected therapeutic genes in plants, animals and humans. (A) induce
XX an effective anti-tumour response without causing harm to the patient.
XX The method uses (A) to generate anti-TAA by exploiting the anti-idiotypic
XX network.
XX SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 20; Length 17;
Best Local Similarity 88.2%; Pred. No. 5.6e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
|||||||:|||||
Db 1 WIDPENGDTYAPKFG 17

RESULT 11
AA97230
ID AAY97230 standard; Protein: 17 AA.
XX AC
XX AAY97230;
XX DT 19-DEC-2000 (first entry)
XX DE Complementary determining region (CDRH2) of anti-SI(KDR) antibody.
XX KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200044777-A1.
XX PD 03-AUG-2000.
XX PF 28-JAN-2000; 2000WO-US02180.
XX PR 29-JAN-1999; 99US-0117726.
XX PR 29-JAN-1999; 99US-0240736.
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z, Witte L;

WPI: 2000-505966/45.
N-PSDB; AAA53762.
Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth

Claim 3; Page 50; 55pp; English.

New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody.
The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Kaposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the immunoglobulins of the invention.

SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-08;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 WIDPENGSDYAPKFG 17
|||||||:|||||
Db 1 WIDPENGSGYAPKFG 17

RESULT 12
AAU74407
ID AAU74407 standard; peptide: 17 AA.
XX AC
XX AAU74407;

DT 26-MAR-2002 (first entry)

XX DE Heavy chain complementarity determining region H2 (CDRH2) version #1.
XX KW Complementary determining region; CDR; CDRH2; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody heavy chain variable domain.

XX OS Mus sp.
XX PN WO200190192-A2.
XX PD 29-NOV-2001.

XX DT 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749p.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX WPI: 2002-106189/14.

XX N-PSDB; AAS20278.

XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides

Claim 55; Page 56; 64pp; English.

The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This peptide sequence represents the heavy chain variable domain complementarity determining region H2 (CDRH2) version #1 incorporated into an antigen-binding protein described in the method of the invention.

SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 23; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
 ||||| ||||| |||||
 Db 1 WIDPENGDSGYAPKFG 17

RESULT 13
 AAY70794
 ID AAY70794 standard; peptide; 20 AA.
 AC AAY70794;
 XX
 XX 31-JUL-2000 (first entry)
 DT
 DE Murine anti-p53 PAB-421 mAb heavy chain CDR based peptide PAB-421 H2.
 XX
 XX Murine; p53 protein; monoclonal antibody; mAb; PAB-421; PAB-421 H2;
 KW heavy chain variable region; VH; complementarity determining region; CDR;
 KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
 KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
 KW DNA-binding domain.
 XX
 OS Mus sp.
 XX
 PN WO200023082-A1.
 XX
 XX 27-APR-2000.
 XX
 XX 19-OCT-1999; 99WO-US24443.
 XX
 XX 19-OCT-1998; 98US-0104816.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;
 PI Wolkowicz R;
 XX
 XX WPI; 2000-339512/29.
 XX
 XX Treatment of systemic lupus erythematosus by down-regulating the
 PT autoimmune response to the C-terminal DNA-binding domain of the p53
 PT protein by an active compound comprising of antibodies to p53 or
 PT fragments of p53 .
 XX
 XX Claim 78; Fig 10; 87pp; English.
 XX
 XX The patent discloses a method for the treatment of systemic lupus
 CC erythematosus (SLE) by down-regulating the autoimmune response to the
 CC C-terminal DNA-binding domain of p53 protein by an active compound.
 CC The present sequence is a PAB-421 H2 peptide which comprises the
 CC complementarity determining region (CDR) of the heavy chain of a
 CC monoclonal antibody PAB-421 which is specific to the C-terminal
 CC DNA-binding domain of murine p53 protein. The peptide corresponds to
 CC residues 48-67 of PAB-421 heavy chain variable region. It is an
 CC example of the active compound useful in the diagnosis, prevention
 CC and treatment of SLE in humans.
 XX
 XX Sequence 20 AA;
 SQ

Query Match 93.1%; Score 94; DB 21; Length 20;
 Best Local Similarity 88.2%; Pred. No. 6.6e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
 ||||| ||||| |||||
 Db 3 WIDPENGDEYAPKFG 19

RESULT 14
 AAW89173
 ID AAW89173 standard; peptide; 112 AA.
 XX
 XX AAW89173;
 AC
 XX

DT 25-MAR-1999 (first entry)
 XX
 DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
 XX
 KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
 KW immune response; tumour associated antigen; metastatic cancer.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO9856416-A1.
 XX
 XX 17-DEC-1998.
 PD
 XX
 PF 09-JUN-1998; 98WO-IL00266.
 XX
 XX 09-JUN-1997; 97IL-0121041.
 PR
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
 PI Wolkowicz R;
 XX
 XX WPI; 1999-070296/06.
 DR
 XX Use of a monoclonal antibody to a tumour-associated antigen - to
 PT induce anti-tumour immunity or elicit an increased immune response
 PT to the antigen
 XX
 XX Example 3; Fig 3; 47pp; English.
 PS
 XX The present invention describes the use of an immunogen (A) to induce
 CC anti-tumour immunity; to elicit an increased immune response to tumour
 CC associated antigen (TAA) and/or to induce an immune response to mutant
 CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
 CC (mAb) to TAA, or its fragment; (ii) a peptide based on a CDR
 CC (complementarity determining region) on the heavy or light chain of MAb
 CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
 CC variable (V) region of MAb, in a gene delivery vehicle. The present
 CC sequence represents the variable heavy chain sequence from anti-p53 MAb
 CC 421. Also described is a method for generating sequence-specific,
 CC anti-DNA antibodies (Ab) by immunising a mammal with a MAb directed to a
 CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
 CC used to treat a wide variety of primary and metastatic cancers,
 CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
 CC to determine critical sequences in animal or plant breeding); to
 CC identify bacteria and other parasites; to determine parentage; in
 CC forensic science; to isolate specific genes for DNA vaccination; in gene
 CC sequencing and cloning; also possibly for activation of selected
 CC therapeutic genes in plants, animals and humans. (A) induce an effective
 CC anti-tumour response without causing harm to the patient. The method
 CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.
 XX
 XX Sequence 112 AA;
 SQ

Query Match 93.1%; Score 94; DB 20; Length 112;
 Best Local Similarity 88.2%; Pred. No. 4.2e-07;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
 ||||| ||||| |||||
 Db 47 WIDPENGDEYAPKFG 63

RESULT 15
 AAY70787
 ID AAY70787 standard; Protein; 116 AA.
 XX
 XX AAY70787;
 AC
 XX 31-JUL-2000 (first entry)
 DT
 XX Murine anti-p53 monoclonal antibody PAB-421 heavy chain variable region.
 DE

XX Murine; p53 protein; monoclonal antibody; PAB-421; DNA-binding domain;
 KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
 KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
 KW heavy chain variable region; VH; complementarity determining region; CDR.
 XX

OS Mus sp.

XX Location/Qualifiers
 XX Key 26...35
 XX Region /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 50...66
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 99...105
 FT /label= CDR
 FT /note= "Complementarity determining region"

XX WO200023082-A1.

XX PD 27-APR-2000.

XX PF 19-OCT-1999; 99WO-US24443.

XX PR 19-OCT-1998; 98US-0104816.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;

XX DR WPI; 2000-339512/29.

XX Treatment of systemic lupus erythematosus by down-regulating the
 PT autoimmune response to the C-terminal DNA-binding domain of the p53
 PT protein by an active compound comprising of antibodies to p53 or
 PT fragments of p53 -

XX Claim 78; Fig 9; 87pp; English.

XX The patent discloses a method for the treatment of systemic lupus
 CC erythematosus (SLE) by down-regulating the autoimmune response to the
 CC C-terminal DNA-binding domain of p53 protein by an active compound.
 CC The present sequence is a heavy chain variable region of monoclonal
 CC antibody PAB-421 which is specific to the C-terminal DNA-binding domain
 CC of murine p53 protein. PAB-421 antibody and peptides based on
 CC complementarity determining regions of light and heavy chain variable
 CC regions of the antibody, are examples of active compounds useful in the
 CC diagnosis, prevention and treatment of SLE in humans.

XX SQ Sequence 116 AA;

Query Match 93.1%; Score 94; DB 21; Length 116;
 Best Local Similarity 88.2%; Pred. NO. 4.4e-07;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDVAPKFGQ 17

DB 50 WIDPENGDTAPKFGQ 66

Search completed: December 23, 2002, 07:25:09
 Job time : 9.12597 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 3.06395 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-21
Perfect score: 101
Sequence: 1 WIDPENGSDYAPKFGQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	93.1	124	1	US-08-017-570-4
2	94	93.1	124	1	US-08-017-570-6
3	94	93.1	124	1	US-08-471-426-4
4	94	93.1	124	1	US-08-471-426-6
5	94	93.1	124	4	US-09-672-609-1
6	94	93.1	124	4	US-09-672-609-3
7	94	93.1	124	4	US-09-672-609-4
8	94	93.1	124	4	US-09-672-609-5
9	94	93.1	124	4	US-09-672-609-6
10	94	93.1	124	4	US-09-672-609-7
11	94	93.1	124	4	US-09-672-609-8
12	94	93.1	124	4	US-09-672-609-9
13	94	93.1	124	4	US-09-672-609-10
14	94	93.1	124	4	US-09-672-609-11
15	94	93.1	124	4	US-09-672-609-12
16	94	93.1	124	4	US-09-025-403A-1
17	94	93.1	124	4	US-09-025-403A-3
18	94	93.1	124	4	US-09-025-403A-4
19	94	93.1	124	4	US-09-025-403A-5
20	94	93.1	124	4	US-09-025-403A-6
21	94	93.1	124	4	US-09-025-403A-7
22	94	93.1	124	4	US-09-025-403A-8
23	94	93.1	124	4	US-09-025-403A-9
24	94	93.1	124	4	US-09-025-403A-10
25	94	93.1	124	4	US-09-025-403A-11
26	94	93.1	124	4	US-09-025-403A-12
27	94	93.1	124	5	PCT-US94-01709-4

28	94	93.1	124	5	PCT-US94-01709-6	Sequence 6, Appli
29	94	93.1	270	2	US-08-652-507-2	Sequence 2, Appli
30	94	93.1	535	4	US-08-983-035A-38	Sequence 38, Appli
31	94	93.1	553	2	US-08-661-052-16	Sequence 16, Appli
32	94	93.1	553	4	US-09-188-082-16	Sequence 16, Appli
33	94	93.1	553	4	US-09-364-088-16	Sequence 16, Appli
34	94	93.1	553	4	US-09-102-716-16	Sequence 16, Appli
35	90	89.1	17	4	US-09-171-945-31	Sequence 31, Appli
36	90	89.1	120	4	US-09-171-945-11	Sequence 11, Appli
37	90	89.1	120	4	US-09-171-945-55	Sequence 55, Appli
38	90	89.1	120	4	US-09-171-945-75	Sequence 75, Appli
39	90	89.1	120	4	US-09-171-945-79	Sequence 79, Appli
40	90	89.1	120	4	US-09-171-945-81	Sequence 81, Appli
41	90	89.1	120	4	US-09-171-945-85	Sequence 85, Appli
42	90	89.1	120	4	US-09-171-945-89	Sequence 89, Appli
43	90	89.1	120	4	US-09-171-945-91	Sequence 91, Appli
44	90	89.1	255	4	US-09-171-945-19	Sequence 19, Appli
45	90	89.1	255	4	US-09-171-945-57	Sequence 57, Appli

ALIGNMENTS

RESULT 1
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-4

Query Match 93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 1 WIDPENGSDYAPKFGQ 17
Db 50 WIDPENGTEYAPKFGQ 66

RESULT 2
US-08-017-570-6
; Sequence 6, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-6

Query Match 93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
DB 50 WIDPENGDTYAPKFG 66

RESULT 3
US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US

ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4

Query Match 93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
DB 50 WIDPENGDTYAPKFG 66

RESULT 4
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match 93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 5

US-09-672-609-1
; Sequence 1, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672.609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-672-609-1

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 6

US-09-672-609-3
; Sequence 3, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672.609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3

; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-3

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 7

US-09-672-609-4
; Sequence 4, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672.609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 4
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVH
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-4

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 8

US-09-672-609-5
; Sequence 5, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672.609
; CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-672-609-5

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGTEYAPKFG 66

RESULT 9
US-09-672-609-6
; Sequence 6, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; FILE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 6
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
US-09-672-609-6

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGTEYAPKFG 66

RESULT 10
US-09-672-609-7
; Sequence 7, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.

; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
US-09-672-609-7

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGTEYAPKFG 66

RESULT 11
US-09-672-609-8
; Sequence 8, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; FILE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 8
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHATAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|||||:|||||
Db 50 WIDPENGTEYAPKFG 66

RESULT 12
US-09-672-609-9
; Sequence 9, Application US/09672609
; Patent No. 6333405

GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 9
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Humanized COL-1 VH, HuVHSTAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
; OTHER INFORMATION: Thr-98
US-09-672-609-9

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 13
US-09-672-609-10
; Sequence 10, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Humanized COL-1 VH, HuVHT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
US-09-672-609-10

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 14
US-09-672-609-11
; Sequence 11, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 11
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Humanized COL-1 VH, HuVHS
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
US-09-672-609-11

Query Match 93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | : | | | | |
Db 50 WIDPENGTEYAPKFG 66

RESULT 15
US-09-672-609-12
; Sequence 12, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 12
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Humanized COL-1 VH, HuVHSTAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC
; OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL-1 VH C
; OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79,
; OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
US-09-672-609-12

Query Match 93.1%; Score 94; DB 4; Length 124;

Best Local Similarity 88.2%; Pred. No. 6.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
|||||||:|||||||
Db 50 WIDPENGTEYAPKFG.66

Search completed: December 23, 2002, 07:33:18
Job time : 3.06395 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 3.36047 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-21

Perfect score: 101

Sequence: 1 WIDPENGSDYAPKFGQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	93.1	82	2 A36025	Ig heavy chain V r
2	86	85.1	118	2 S25174	Ig heavy chain V r
3	84	83.2	136	2 S04576	Ig heavy chain pre
4	82	81.2	116	2 S15672	Ig heavy chain V r
5	78	77.2	137	2 S52445	Ig heavy chain V r
6	68	67.3	143	1 E1HUND	Ig heavy chain pre
7	67	66.3	85	2 E37262	Ig heavy chain V r
8	64	63.4	86	2 S54912	Ig heavy chain V r
9	63	62.4	98	2 S26938	Ig heavy chain V r
10	63	62.4	98	2 S26912	Ig heavy chain V r
11	63	62.4	99	2 D37262	Ig heavy chain V r
12	63	62.4	107	2 PH1013	Ig heavy chain V r
13	63	62.4	108	2 PH1012	Ig heavy chain V r
14	63	62.4	117	2 S31680	Ig heavy chain V r
15	63	62.4	117	2 S18551	Ig heavy chain V r
16	63	62.4	118	2 S36285	Ig heavy chain V r
17	63	62.4	120	2 S03471	Ig heavy chain V-D
18	63	62.4	122	2 S06823	Ig heavy chain V r
19	63	62.4	123	2 D33548	Ig heavy chain V-1
20	63	62.4	123	2 PH1403	Ig heavy chain V r
21	63	62.4	129	2 S46393	Ig heavy chain V r
22	63	62.4	135	2 S49530	anti-Sm antibody V
23	62	61.4	178	2 S29594	Ig gamma chain (WM
24	61	60.4	120	2 S03484	Ig heavy chain V-D
25	61	60.4	221	2 S49220	Ig gamma-1 chain -
26	60	59.4	77	2 S46455	Ig heavy chain V r
27	60	59.4	98	2 S26918	Ig heavy chain V r
28	60	59.4	98	2 S26909	Ig heavy chain V r
29	60	59.4	132	2 S31596	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A36025

Ig heavy chain V region (PR8-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999

C:Accession: A36025; E36025

R:Caton, A.J.; Koprowski, H.

Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990

A:Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinator
A:Reference number: A36025; MUID:90349634; PMID:1696733

A:Accession: A36025

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-82 <CA2>

A:Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956

A:Note: PR8-1

A:Accession: E36025

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 19-82 <CA2>

A:Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964

A:Note: clone PR8-21

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 82;

Best Local Similarity 88.2%; Pred. No. 5.9e-08;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFGQ 17

Db 12 WIDPENGDTYAPKFGQ 28

RESULT 2

S25174

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S25174; S33133

R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.

submitted to the EMBL Data Library, July 1992

A:Description: Structure and binding properties of monoclonal antibodies to core hist

A:Reference number: S25174

A:Accession: S25174

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MON>

A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259

A:Accession: S33133

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MO2>
A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 86; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 1.7e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17
Db 50 WIDPENGDTYASKFOG 66

RESULT 3

S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04576
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: involve
A:Reference number: S04573; MUID:87133856; PMID:3102255
A:Accession: S04576
A:Molecule type: mRNA
A:Residues: 1-136 <KOF>
A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 84; DB 2; Length 136;
Best Local Similarity 82.4%; Pred. No. 4.1e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17
Db 69 WIDPENGDTYASKFOG 85

RESULT 4

S15672
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S15672
R:Tempest, P.R.; Brenner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,
Bio/Technology 9, 266-271, 1991
A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi
A:Reference number: S15672; MUID:91337412; PMID:1367535
A:Accession: S15672
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-116 <TEM>
A:Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 7.2e-06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17
Db 50 WIDPENGDTYASKFOG 66

RESULT 5

us-09-865-198-21.rpr

S52445
Ig heavy chain V region precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52445
R:Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged
A:Reference number: S52445
A:Accession: S52445
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <BER>
A:Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-115/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 78; DB 2; Length 137;
Best Local Similarity 76.5%; Pred. No. 3.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17
Db 69 WIDPENGTVYDPKFOG 85

RESULT 6

EHUND
Ig heavy chain precursor V-I region (ND) - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C:Accession: A93933; A02026
R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: A93933
A:Molecule type: mRNA
A:Residues: 1-143 <KEN>
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.

A:Reference number: A94418
A:Contents: annotation; partial sequence
A:Note: this epsilon chain was isolated from a myeloma protein
C:Genetics:
A:Gene: GDB:IGHV6
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-143/Product: Ig heavy chain V-I region (ND) #status predicted <MAT>
F:30-113/Domain: immunoglobulin homology <IMM>
F:16/Modified site: pyrrolidone carboxylic acid
F:37-111/Disulfide bonds: #status experimental

Query Match 67.3%; Score 68; DB 1; Length 143;
Best Local Similarity 58.8%; Pred. No. 0.0016; 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17
Db 65 WINPNSGGTYAPRFOG 81

RESULT 7

E37262
Ig heavy chain V region (GH2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-May-1997

C;Accession: E37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: E37262
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-85 <GOS>
A;Cross-references: GB:M57991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.3%; Score 67; DB 2; Length 85;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 17
||| ||| : ||| |||
Db 29 IDPANGDTRYPKFG 44

RESULT 8
S54912
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S54912
R;Tomlinson, M.; Walter, G.; Cook, X.Y.2.; Winter, G.
submitted to the EMBL data Library, November 1992
A;Reference number: S54912
A;Accession: S54912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <TOM>
A;Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 86;
Best Local Similarity 64.7%; Pred. No. 0.0036;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
||| ||| : ||| |||
Db 38 WINPENGSPYAKFG 54

RESULT 9
S26938
Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0066;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17

Db 50 WINPNSGGTNYAQKFG 66
||| ||| : ||| |||
RESULT 10
S26912
Ig heavy chain V region (DP-8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12310; NID:g32979; PIDN:CAA78180.1; PID:g32980
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0066;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
||| ||| : ||| |||
Db 50 WINPNSGGTNYAQKFG 66

RESULT 11
D37262
Ig heavy chain V region (2E5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: D37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: D37262
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-99 <GOS>
A;Cross-references: GB:M57990; NID:g195046; PIDN:AAA63328.1; PID:g195047
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 99;
Best Local Similarity 58.8%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 17
||| ||| : ||| |||
Db 43 IDPANGTKYDPKFG 58

RESULT 12
PH1013
Ig heavy chain V region (clone 111.67) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1013
R;Tillman, D.M.; Jow, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1013
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA

A:Residues: 1-107 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 107;
Best Local Similarity 73.3%; Pred. No. 0.0073;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 16
||| ||| : |||||
Db 51 IDPANGNTYAPKFG 65

RESULT 13

PH1012 Ig heavy chain V region (clone 17p.73) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1012
R:Fillman, D.M.; Jow, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1012

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-108 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 108;
Best Local Similarity 73.3%; Pred. No. 0.0073;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 16
||| ||| : |||||
Db 51 IDPANGNTYAPKFG 65

RESULT 14

S31680 Ig heavy chain V region - human

C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31680
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31680

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <CUI>

A:Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796

C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 117;
Best Local Similarity 58.8%; Pred. No. 0.008;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
||| ||| : |||||
Db 69 WINPNSGGTNYAKFG 85

RESULT 15

S18551

Ig heavy chain V region precursor (VI-2) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S23625
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.
EMBO J. 10, 3641-3645, 1991

A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus:
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551

A:Molecule type: DNA

A:Residues: 1-117 <SHI>

A:Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.
J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23625

A:Molecule type: DNA

A:Residues: 1-117 <OLE>

A:Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553

C:Genetics: 16/1

A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 117;
Best Local Similarity 58.8%; Pred. No. 0.008;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17

Db 69 WINPNSGGTNYAKFG 85

Search completed: December 23, 2002, 07:31:39
Job time : 4.36047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 1.68023 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-21

Perfect score: 101

Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	68	67.3	147	1 HV1C_HUMAN	P01744 homo sapien
2	52	51.5	117	1 HV1G_HUMAN	P23083 homo sapien
3	51	50.5	117	1 HV1B_HUMAN	P01743 homo sapien
4	51	50.5	350	1 NUD9_HUMAN	Q9bw91 homo sapien
5	47	46.5	1709	1 SN_HUMAN	Q9bzz2 homo sapien
6	46	45.5	117	1 HV12_MOUSE	P01756 mus musculu
7	46	45.5	117	1 HV13_MOUSE	P01757 mus musculu
8	46	45.5	117	1 HV52_MOUSE	P06327 mus musculu
9	46	45.5	118	1 HV51_MOUSE	P06330 mus musculu
10	45	44.6	1387	1 PUR4_ARATH	Q9m8d3 arabidopsis
11	44	43.6	402	1 MCE1_SCHPO	P40997 schizosacch
12	44	43.6	944	1 CHS2_NEUCR	P30589 neurospora
13	43	42.6	120	1 HV03_MOUSE	P01747 mus musculu
14	43	42.6	238	1 Y1GB_ECOLI	P23306 escherichia
15	43	42.6	511	1 PUR4_SOLME	P37124 solanum mel
16	43	42.6	776	1 HYPE_AZOVI	P40596 azotobacter
17	43	42.6	977	1 DLP3_RAT	P97838 rattus norv
18	43	42.6	3329	1 BRC2_MOUSE	P97929 mus musculu
19	42	41.6	140	1 HV02_MOUSE	P01746 mus musculu
20	41.5	41.1	117	1 HV03_CAICR	P33982 calman croc
21	41.5	41.1	551	1 YG1F_YEAST	P33214 saccharomyc
22	41.5	41.1	597	1 EYFD_CAEEL	Q11190 c probable
23	41	40.6	117	1 HV06_MOUSE	P01750 mus musculu
24	41	40.6	120	1 HV50_MOUSE	P06329 mus musculu
25	41	40.6	526	1 THRC_ARATH	Q9s7b5 arabidopsis
26	41	40.6	783	1 HELS_HALN1	Q9hm66 halobacteri
27	41	40.6	830	1 SREC_HUMAN	Q14162 homo sapien
28	41	40.6	977	1 DLP1_HUMAN	O14490 homo sapien
29	41	40.6	992	1 DLP1_RAT	P97836 rattus norv
30	41	40.6	1005	1 EPAB_HUMAN	P29322 homo sapien
31	41	40.6	1338	1 PUR4_HUMAN	O15067 homo sapien
32	41	40.6	1343	1 PUR4_CAEEL	Q19311 caenorhabdi
33	41	40.6	1354	1 PUR4_DROME	P35421 drosophila

34	41	40.6	1857	1 PAS2_PENPA	P15368 p fatty aci
35	40.5	40.1	205	1 DNBI_ADEL2	P36704 human adeno
36	40	39.6	117	1 HV1A_HUMAN	P01742 homo sapien
37	40	39.6	156	1 RNP_HUMAN	P07998 homo sapien
38	40	39.6	227	1 YG24_HAEIN	P44276 haemophilus
39	40	39.6	254	1 MOX1_HUMAN	P50221 homo sapien
40	40	39.6	297	1 YMY9_YEAST	Q03161 saccharomyc
41	40	39.6	416	1 PAI2_RAT	P29524 rattus norv
42	40	39.6	496	1 PACR_MOUSE	P70205 mus musculu
43	40	39.6	523	1 PACR_RAT	P32215 rattus norv
44	40	39.6	712	1 GFAL_CANAL	P53704 candida alb
45	40	39.6	717	1 MTO1_HUMAN	Q9y2z2 homo sapien

ALIGNMENTS

```
RESULT 1
HV1C_HUMAN          STANDARD;          PRT;    147 AA.
AC      P01744;
DT      21-JUL-1986 (Rel. 01, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ig heavy chain V-I region ND precursor (Fragments).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=83065234; PubMed=6815656;
RA      Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA      Bell L.O., Gould H.J.;
RT      "Cloning and sequence determination of the gene for the human
RT      immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN      [2]
RP      SEQUENCE OF 20-147.
RA      Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL      (In) Bach M.K. (eds.);
RL      Immediate hypersensitivity: modern concepts and developments, pp.1-36,
CC      Marcel Dekker, New York (1978).
CC      -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC      PROTEIN.
DR      PIR: A02026; ELHUND.
DR      HSSP; P01789; IMCP.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; Igv; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL
FT      CHAIN
FT      MOD_RES
FT      DISULFID
FT      CONFLICT
FT      CONFLICT
FT      CONFLICT
FT      CONFLICT
FT      NON_TER
SQ      SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;
      19
      20 147
      20 20
      41 115
      21 21
      53 54
      67 68
      125 125
      147 147
      T -> V (IN REF. 2).
      IH -> HI (IN REF. 2).
      VG -> GV (IN REF. 2).
      MISSING (IN REF. 2).
```

Query Match 67.3%; Score 68; DB 1; Length 147;
Best Local Similarity 58.8%; Pred. NO. 0.00083;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WIDPENGSDYAPKFG 17

||:|:|:|:|:|:|

Db 69 WINPNSGGTNYAPRFQ 85

RESULT 2


```

DR  MIM; 606022;
DR  InterPro; IPR000086; NUDIX_hydrolase.
DR  Pfam; PF00293; NUDIX; 1.
DR  PROSITE; PS00893; NUDIX; 1.
KW  Hydrolase.
FT  DOMAIN 215 237 NUDIX BOX.
SQ  SEQUENCE 350 AA; 39125 MW; 2EA3524B88FB3420 CRC64;

Query Match 50.5%; Score 51; DB 1; Length 350;
Best Local Similarity 46.7%; Pred No. 1;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKF 15
    I I I : : : : I I I
Db 110 WADPQISENFSPEKF 124

RESULT 5
SN_HUMAN
ID SN_HUMAN STANDARD; PRT; 1709 AA.
AC Q9BZ62; Q9H1H7; Q9H7L7; Q9GZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sialoadhesin precursor (Sialic acid binding Ig-like lectin-1) (Siglec-1) (CD169 antigen).
DE GN SN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Hartnell A., Steel J., Turley H., Jones M., Jackson D., Crocker P.R.;
RT "Characterisation of human sialoadhesin (siglec-1), a sialic acid binding receptor expressed on resident and inflammatory macrophage populations."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.B., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE OF 733-1709 FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Spleen;
RA Ohara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human

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RT spleen."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MACROPHAGE-RESTRICTED ADHESION MOLECULE THAT MEDIATES
CC SIALIC-ACID DEPENDENT BINDING TO CELLS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
CC SOLUBLE (ISOFORM 2).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- DATABASE: NAME=PROW; NOTE=PROW 2:18-22(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/985165905-g.htm".
CC -----
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CC -----
CC EMBL; AF230073; AAK00757.1; -
CC EMBL; ALI09804; CAC17543.1; -
CC EMBL; ALI09804; CAC17542.1; -
CC EMBL; AK024462; BAB15752.1; -
CC EMBL; AK024459; BAB15749.1; -
CC EMBL; AK024479; BAB15769.1; -
CC HSSP; Q62230; IQFO.
CC Genew; HGNC:11127; SN.
CC MIM; 600751; -
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003600; Ig_Like.
CC Pfam; PF00047; Ig; 14.
CC SMART; SM00409; IG; 17.
CC SMART; SM00410; IG_Like; 1.
CC SMART; SM00408; IGC2; 14.
KW Signal; Glycoprotein; Cell adhesion; Immunoglobulin domain; Repeat;
KW Transmembrane; Alternative splicing; Antigen.
FT SIGNAL 1 19
FT CHAIN 20 1709
FT DOMAIN 20 1641
FT TRANSSEM 1642 1662
FT DOMAIN 1663 1709
FT DOMAIN 20 136
FT DOMAIN 153 224
FT DOMAIN 255 312
FT DOMAIN 339 397
FT DOMAIN 426 498
FT DOMAIN 524 582
FT DOMAIN 617 696
FT DOMAIN 722 781
FT DOMAIN 810 883
FT DOMAIN 909 967
FT DOMAIN 998 1074
FT DOMAIN 1100 1156
FT DOMAIN 1186 1248
FT DOMAIN 1274 1331
FT DOMAIN 1360 1432
FT DOMAIN 1458 1518
FT DOMAIN 1547 1620
FT DISULFID 41 98
FT DISULFID 160 217
FT DISULFID 262 305
FT DISULFID 346 390
FT DISULFID 433 491
FT DISULFID 531 575
FT DISULFID 624 689
FT DISULFID 729 774
FT DISULFID 817 876
FT DISULFID 916 960

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FT DISULFID 1005 1067 BY SIMILARITY.
FT DISULFID 1107 1149 BY SIMILARITY.
FT DISULFID 1193 1241 BY SIMILARITY.
FT DISULFID 1281 1324 BY SIMILARITY.
FT DISULFID 1367 1425 BY SIMILARITY.
FT DISULFID 1465 1511 BY SIMILARITY.
FT DISULFID 1534 1613 BY SIMILARITY.
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 697 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 730 730 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 741 741 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 886 886 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1104 1104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1138 1138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1251 1251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1462 1462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1476 1476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1632 1709 ALHRLHFOQLLWVIGLLVGLLLGLGACVWRRRVCK
QMSGNSVEMAFQKETTQLIDPDATCETSTCAPPLG ->
GGGRGLHLPGHSAQKPS (IN ISOFORM 2).
A -> T (IN REF. 1).
A -> V (IN REF. 3; BAB15749/BAB15769).
SQ SEQUENCE 1709 AA; 182624 MW; 587C7CCA0B789A6D CRC64;

Query Match 46.5%; Score 47; DB 1; Length 1709;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 NGDSYAPKFG 17
:||||:|:|
DB 456 SGDSHSPRFG 467

RESULT 6
HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry W.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFG 17
|:| | | : | | | |
DB 51 INPNGGTSYNOKFKG 66

RESULT 7
HV13_MOUSE STANDARD; PRT; 117 AA.
ID HV13_MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFG 17
|:| | | : | | | |
DB 51 INPNGGTSYNOKFKG 66

RESULT 8
HV52_MOUSE STANDARD; PRT; 117 AA.
ID HV52_MOUSE
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT rearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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DR EMBL; X77782; CAAS4816.1; -;
DR EMBL; M82951; AAA33582.1; -;
DR PIR; B45189; B45189;
DR InterPro; IPR004834; Chitin synth.
DR Pfam; PF01644; Chitin synth; 1.
DR ProDom; PD002998; Chitin synth; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Cell wall;
KW Multigene family.
FT TRANSMEM 597 617 POTENTIAL.
FT TRANSMEM 634 654 POTENTIAL.
FT TRANSMEM 669 689 POTENTIAL.
FT TRANSMEM 713 733 POTENTIAL.
FT TRANSMEM 873 893 POTENTIAL.
SQ SEQUENCE 944 AA; 106816 MW; F70052AE0803060D CRC64;

Query Match 43.6%; Score 44; DB 1; Length 944;
Best Local Similarity 47.1%; Pred. No. 39;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17
|| : ||: ||: ||:
Db 917 WIREKMGDADVKGKFE 933

RESULT 13

HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVMSG7.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsenate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 42.6%; Score 43; DB 1; Length 120;
Best Local Similarity 47.1%; Pred. No. 5.8;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17
: || || : ||: ||:
Db 49 YINPGNGYTKYNEKFG 65

RESULT 14

YIGB_ECOLI

ID YIGB_ECOLI STANDARD; PRT; 238 AA.
AC P23306; P76757;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yigB.
GN YIGB OR B3812.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RT from 84.5 to 86.5 minutes.";
RL Science 257:771-778(1992).
RN [2]
RP REVISION TO 13.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=91072248; PubMed=2254268;
RA Colloms S.D., Sykora P., Szatmari G., Sherratt D.J.;
RT "Recombination at ColE1 cer requires the Escherichia coli xerC gene
RT product, a member of the lambda integrase family of site-specific
RT recombinases.";
RL J. Bacteriol. 172:6973-6980(1990).
RN [4]
RP SEQUENCE OF 183-238 FROM N.A.
RX MEDLINE=84272253; PubMed=6379604;
RA Finch P.W., Emmerson P.T.;
RT "The nucleotide sequence of the uvrD gene of E. coli.";
RL Nucleic Acids Res. 12:5789-5799(1984).
RN [5]
RP SEQUENCE OF 183-238 FROM N.A.
RX MEDLINE=84169504; PubMed=6324092;
RA Easton A.M., Kushner S.R.;
RT "Transcription of the uvrD gene of Escherichia coli is controlled by
RT the LexA repressor and by attenuation.";
RL Nucleic Acids Res. 11:8625-8640(1983).
CC -1- SIMILARITY: TO E.COLI YJ3G.
CC -----
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DR EMBL; M87049; AAA67608.1; -;

DR EMBL; AS000457; AAC76815.1; -;

DR EMBL; M38257; AAA24764.1; -;

DR EMBL; X00738; -; NOT_ANNOTATED_CDS.

DR PIR; D37841; D37841.

DR PIR; S30702; S30702.

DR EcoGene; EGI1202; yigB.

DR InterPro; IPR001454; Hlgnsase/hydrlase.

DR Pfam; PF00702; Hydrolase; 1.

KW Hypothetical protein; Complete proteome.

FT CONFLICT 13 13 L -> V (IN REF. 1).

FT CONFLICT 200 200 S -> T (IN REF. 3).

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SQ SEQUENCE 238 AA: 27122 MW; 9C1BDE710641E0D6 CRC64;
Query Match 42.6%; Score 43; DB 1; Length 238;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENG D 8
   || || || || ||
Db 206 WIRPENG D 213

RESULT 15
C772_SOLME
ID C772_SOLMER STANDARD; PRT; 511 AA.
AC P37124;
DT 01-OCT-1998 (Rel. 30, Created)
DT 01-OCT-1998 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytochrome P450 77A2 (EC 1.14.-.-) (CYPLXXVIIA2) (P-450EG5).
GN CYP77A2 OR CYPEG5.
OS Solanum melongena (Eggplant) (Aubergine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sinsadoharanasu; TISSUE=Hypocotyl;
RX MEDLINE=94013942; PubMed=8307197;
RA Toguri T. Tokugawa K.;
RT "Cloning of eggplant hypocotyl cDNAs encoding cytochromes P450
RL FEBS Lett. 338:290-294(1994).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
-----
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-----
CC EMBL; X71655; CAA50646.1; -.
DR PIR; S41598;
DR PIR; S40266; S40266.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Heme; Multigene family.
FT BINDING 456 456 HEME (BY SIMILARITY)
SQ SEQUENCE 511 AA; 58114 MW; 4B2A185D4DAFE023 CRC64;

Query Match 42.6%; Score 43; DB 1; Length 511;
Best Local Similarity 43.8%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPK FQ 16
   | | | | | | |
Db 479 WADPENTRVDFTEKLE 494

Search completed: December 23, 2002, 07:26:13
Job time : 3.68023 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 7.05039 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-21

Perfect score: 101

Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	76	75.2	468	11	Q99L31	Q99L31 mus musculus
2	60	59.4	497	4	Q8WZ24	Q8WZ24 homo sapien
3	59	58.4	614	4	Q96GA6	Q96GA6 homo sapien
4	58	57.4	109	11	Q9JL85	Q9JL85 mus musculus
5	57.5	56.9	150	4	Q9Y298	Q9Y298 homo sapien
6	56	55.4	125	4	Q9UL95	Q9UL95 homo sapien
7	55	54.5	119	4	Q9UL94	Q9UL94 homo sapien
8	54	53.5	481	11	Q8VCV5	Q8VCV5 mus musculus
9	51	50.5	124	4	Q9UL92	Q9UL92 homo sapien
10	51	50.5	300	11	Q9D0U2	Q9D0U2 mus musculus
11	51	50.5	350	4	Q96KB3	Q96KB3 homo sapien
12	50	49.5	500	4	Q9BRV0	Q9BRV0 homo sapien
13	48.5	48.0	474	11	Q8R3H6	Q8R3H6 mus musculus
14	48	47.5	102	11	Q9JL79	Q9JL79 mus musculus
15	48	47.5	147	11	Q925S3	Q925S3 mus musculus
16	48	47.5	323	10	Q9STS2	Q9STS2 arabidopsis

17	48	47.5	379	10	Q8RYD8	Q8RYD8 arabidopsis
18	48	47.5	403	16	Q8YU7	Q8YU7 ralstonia s
19	48	47.5	484	11	Q99LA6	Q99LA6 mus musculus
20	48	47.5	526	17	Q8TJE3	Q8TJE3 methanosarc
21	47	46.5	481	11	Q91WT1	Q91WT1 mus musculus
22	47	46.5	520	11	Q921T2	Q921T2 mus musculus
23	46	45.5	117	11	Q9QXF0	Q9QXF0 mus musculus
24	46	45.5	117	11	Q9QXE9	Q9QXE9 mus musculus
25	46	45.5	159	4	Q96QSO	Q96QSO homo sapien
26	46	45.5	1737	11	Q9JIC4	Q9JIC4 rattus norv
27	45.5	45.0	118	11	Q9ZIC4	Q9ZIC4 mus musculus
28	45	44.6	138	2	Q9F8N0	Q9F8N0 carboxydoth
29	45	44.6	168	17	Q27394	Q27394 methanobact
30	45	44.6	179	10	Q9XI82	Q9XI82 arabidopsis
31	45	44.6	318	10	Q9LWF3	Q9LWF3 arabidopsis
32	45	44.6	348	5	Q16334	Q16334 caenorhabdi
33	45	44.6	1289	10	Q8VYU2	Q8VYU2 vigna ungu
34	44.5	44.1	462	16	Q8Y074	Q8Y074 ralstonia s
35	44	43.6	219	16	Q34915	Q34915 bacillus su
36	44	43.6	224	9	Q64131	Q64131 bacterioph
37	44	43.6	224	16	Q31916	Q31916 bacillus su
38	44	43.6	234	10	Q9STK0	Q9STK0 arabidopsis
39	44	43.6	238	10	Q93WL3	Q93WL3 arabidopsis
40	44	43.6	249	16	Q69834	Q69834 streptomyce
41	44	43.6	317	17	Q9YD93	Q9YD93 aeropyrum p
42	44	43.6	387	10	Q9SHD8	Q9SHD8 arabidopsis
43	44	43.6	392	10	Q9SLA1	Q9SLA1 arabidopsis
44	44	43.6	488	11	Q9LWR1	Q9LWR1 mus musculus
45	44	43.6	687	10	Q9LHA3	Q9LHA3 arabidopsis

ALIGNMENTS

RESULT 1

Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 75.2%; Score 76; DB 11; Length 468;

Best Local Similarity 75.0%; Pred. No. 0.00095;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 16

Db 69 WIDPEDGETKYAPKFG 84

```
RESULT 2
Q8WY24          PRELIMINARY;      PRT;    497 AA.
ID Q8WY24
AC Q8WY24
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SCN66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SNC66, a Ig-like gene which is
  down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IG1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A63E5 CRC64;

Query Match          59.4%; Score 60; DB 4; Length 497;
Best Local Similarity 47.1%; Pred. No. 0.35;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
|:::|:::|:::|
Db 69 WNNPOTGNTFEAQKFG 85

RESULT 3
Q96GA6          PRELIMINARY;      PRT;    614 AA.
ID Q96GA6
AC Q96GA6
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Unknown protein for MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00041; HTHARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match          58.4%; Score 59; DB 4; Length 614;
Best Local Similarity 62.5%; Pred. No. 0.64;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 16
|:::|:::|:::|

RESULT 4
Q9JL85          PRELIMINARY;      PRT;    109 AA.
ID Q9JL85
AC Q9JL85
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
  (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALE/C;
RC MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
  streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
  with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match          57.4%; Score 58; DB 11; Length 109;
Best Local Similarity 68.8%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFG 17
|:::|:::|:::|
Db 43 IDPATGHSKYDPKFG 58

RESULT 5
Q9Y298          PRELIMINARY;      PRT;    150 AA.
ID Q9Y298
AC Q9Y298
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Igg VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacquemin M.G., Vander Elst L.P.L.;
RC MEDLINE=98322155; PubMed=9657749;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
  IgG4 monoclonal antibody derived from a hemophilia A patient with
  inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
```


FT SIGNAL 1 19 POTENTIAL.
SQ NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;
Query Match 56.98; Score 57.5; DB 4; Length 150;
Best Local Similarity 55.08; Pred. No. 0.21;
Matches 11; Conservative 4; Mismatches 2; Indels 3; Gaps 1;
QY 1 WI---DPENGSDYAPKFG 17
I: |||:|:|:|:|:|
Db 66 WVGSDPESGESIYAREFG 85
RESULT 6
Q9UL95
ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -;
DR HSSP: P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
Query Match 55.48; Score 56; DB 4; Length 125;
Best Local Similarity 52.98; Pred. No. 0.29;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
||:|:|:|:|:|
Db 50 WINPNSGGTNYAQKVG 66
RESULT 7
Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035020; AAD56256.1; -;
DR HSSP: P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
Query Match 54.58; Score 55; DB 4; Length 119;
Best Local Similarity 52.98; Pred. No. 0.4;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
||:|:|:|:|:|
Db 50 WINPNSWTTNYAQKFG 66
RESULT 8
Q8VCV5
ID Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC018455; AAH18455.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 3.
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;
Query Match 53.58; Score 54; DB 11; Length 481;
Best Local Similarity 58.88; Pred. No. 3;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 WIDPENGSDYAPKFG 17
:|||:|:|:|:|:|
Db 69 YIDPYNGGSYNAQKFG 85
RESULT 9
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

Qy 1 WIDPENGSDSYAPKPF 15
I ||| :||:||||
Db 60 WADPQISENFSFKF 74

RESULT 11

Q96KB3 PRELIMINARY; PRT; 350 AA.

AC Q96KB3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CDNA FLJ14389 fis, clone HEMBA1002876.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=EMBRYO, AND MAINLY HEAD;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Takiguchi
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Nanomiya K., Iwavanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK021295; BAB5021.1;
DR InterPro: IPR000086; NUDIX_hydrolase.
DR Pfam: PF00293; NUDIX; 1.
SQ SEQUENCE 350 AA; 39042 MW; 8BE1A31ECCFB343D CRC64;

Query Match 50.5%; Score 51; DB 4; Length 350;
Best local similarity 46.7%; Pred. No. 6.1;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WIDPENGSDSYAPKPF 15
I ||| :||:||||
Db 110 WADPQISENFSFKF 124

RESULT 12

Q9BRV0 PRELIMINARY; PRT; 500 AA.

AC Q9BRV0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 54.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC005951; AAH05951.1;
DR HSSP; P01789; IMCP.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-1.
DR InterPro: IPR003606; Ig-MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig. 4.
DR SMART; SM00409; Ig. 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IgV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 49.5%; Score 50; DB 4; Length 500;
Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
||| : : : ||||
Db 69 WISPSDNTREAKKFG 85

RESULT 13

ID Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAK25447.1; -.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 48.0%; Score 48.5; DB 11; Length 474;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 10; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

Qy 1 WID---PENGSDYAPKFG 17
||| : : : ||||
Db 66 WIGRIFPGDGDTHYSGKFG 85

RESULT 14

ID Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR HSSP; P01772; 2FE4
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 47.5%; Score 48; DB 11; Length 102;
Best Local Similarity 47.1%; Pred. No. 4.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
||| : : : ||||
Db 35 WINTETGEPTYADDFKG 51

RESULT 15

ID Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Ren D., Zhao T., Li X., Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/C;
RX Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 47.5%; Score 48; DB 11; Length 147;
Best Local Similarity 47.1%; Pred. No. 6.6;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
||| : : : ||||
Db 52 WIFPGEGSTEYNEKFKG 68

Search completed: December 23, 2002, 07:29:58
Job time : 9.05039 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 21.0872 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVRLQSGAELVSGASVKL.....AYYGDYRGYWGQGTIVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558.5	88.5	535	4	US-08-983-035A-38
2	536.5	85.0	118	3	US-08-767-128-22
3	517.5	82.0	270	2	US-08-652-507-2
4	511.5	81.1	124	1	US-08-017-570-6
5	511.5	81.1	124	1	US-08-471-426-6
6	511.5	81.1	124	5	PCT-US94-01709-6
7	511.5	81.1	553	2	US-08-661-052-16
8	511.5	81.1	553	4	US-09-188-082-16
9	511.5	81.1	553	4	US-09-364-088-16
10	511.5	81.1	553	4	US-09-102-716-16
11	506.5	80.3	124	1	US-08-017-570-4
12	506.5	80.3	124	1	US-08-471-426-4
13	506.5	80.3	124	5	PCT-US94-01709-4
14	503.5	79.8	124	4	US-09-672-609-1
15	503.5	79.8	124	4	US-09-025-403A-1
16	502.5	79.6	281	4	US-09-423-439-44
17	502.5	79.6	642	4	US-09-423-439-26
18	502.5	79.6	666	4	US-09-423-439-51
19	499.5	79.2	250	4	US-09-171-945-19
20	484.5	76.8	120	4	US-09-171-945-11
21	481.5	76.3	136	4	US-08-348-548-8
22	481.5	76.3	136	5	PCT-US95-15716-8
23	481.5	76.2	125	2	US-08-561-521-44
24	481.5	76.2	125	5	PCT-US95-01219-44
25	478.5	75.8	117	2	US-08-290-592E-18
26	478.5	75.8	117	5	PCT-US95-10053-15
27	478.5	75.8	117	5	PCT-US96-09448-18

28	476	75.4	136	4	US-08-646-265A-29	Sequence 29, Appl
29	471.5	74.7	118	2	US-08-232-081B-38	Sequence 38, Appl
30	469	74.3	123	2	US-08-561-521-9	Sequence 9, Appl
31	469	74.3	123	5	PCT-US95-01219-9	Sequence 9, Appl
32	467	74.0	121	2	US-08-822-830B-13	Sequence 13, Appl
33	464	73.5	121	2	US-08-822-830B-2	Sequence 2, Appl
34	462	73.2	120	2	US-08-950-660-2	Sequence 2, Appl
35	462	73.2	120	5	PCT-US93-00030-2	Sequence 2, Appl
36	462	73.2	120	5	PCT-US93-00924-2	Sequence 2, Appl
37	461	73.1	140	2	US-08-561-521-4	Sequence 4, Appl
38	461	73.1	140	5	PCT-US95-01219-4	Sequence 4, Appl
39	459	72.7	136	1	US-08-024-253-2	Sequence 2, Appl
40	456	72.3	254	2	US-08-792-824-4	Sequence 4, Appl
41	456	72.3	254	2	US-08-792-824-7	Sequence 7, Appl
42	456	72.3	254	2	US-08-792-824-10	Sequence 10, Appl
43	456	72.3	254	2	US-08-792-824-13	Sequence 13, Appl
44	451.5	71.6	120	4	US-08-871-488A-15	Sequence 15, Appl
45	448.5	71.1	113	1	US-08-207-169A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-983-035A-38
; Sequence 38, Application US/08983035A
; Patent No. 6326464
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,035A
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01111
; FILING DATE: 17-JUL-1996
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Strauss, William L.
; REGISTRATION NUMBER: 47,114
; REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38
Query Match 88.5%; Score 558.5; DB 4; Length 535;
Best Local Similarity 88.9%; Pred. No. 6.5e-49;


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: CITY: Midland
: STATE: MI
: COUNTRY: US
: ZIP: 48641-1967
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/471,426
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/017,570
: FILING DATE: 16-FEB-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: ULMER, DUANE C
: REGISTRATION NUMBER: 34,941
: REFERENCE/DOCKET NUMBER: C-38,777
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (517) 636-8104
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 124 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-471-426-6

Query Match      81.1%; Score 511.5; DB 1; Length 124
Best Local Similarity 77.2%; Pred. No. 6.7e-45;
Matches 98; Conservative 9; Mismatches 7; Indels 1

QY      1 QVKLQSGAELVSGASVKLSCTTSFGFNKDFYMHVYKQRPQGLEWIGWIDPEN
Db      1 EVOLQSGAELVSRGASVKMSC*FASGFNKKDYMHVYKQRPQGLEWIGWIDPEN
QY      61 APKFOCKATMTADSSNTAYLQLSSLTSEDYAVYCNAAAAAAAAAAAAAAAAAAAA
Db      61 APKFOCKATMTDTSNTAYLQLSSLTSEDYAVYCNTRLGSLMTWTRWFFD---
QY      111 TTVTVSS 117
Db      118 TTVTVSS 124

RESULT 6
PCT-US94-01709-6
: Sequence 6, Application PC/TUS9401709
: GENERAL INFORMATION:
: APPLICANT: THE DOW CHEMICAL COMPANY
: APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
: TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
: TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Duane C. Ulmer
: STREET: P.O. Box 1967
: CITY: Midland
: STATE: MI
: COUNTRY: US
: ZIP: 48641-1967
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/01709
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:

```

NAME: UEMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01709-6

Query Match 81.1%; Score 511.5; DB 5; Length 124;
Best Local Similarity 77.2%; Pred. No. 6.7e-45;
Matches 98; Conservative 9; Mismatches 7; Indels 13; Gaps 2;

QY 1 QVQLQSGAELVSGASVKLSCTTSGFNIKDFYMHVWKORPEQGLEWIDPENGDSY 60
Db 1 EVQLQSGAELVSGASVKLSCTTSGFNIKDFYMHVWKORPEQGLEWIDPENGDT 60
QY 61 APFGKATMTADSSNTAYLQLSLTSETAVYYCNA-----YGDYEGYWGQ 110
Db 61 APFGKATMTDTSSNTAYLQLSLTSETAVYYCNRGLSTMTITRFFD---VMGAG 117
QY 111 TTVTVSS 117
Db 118 TTVTVSS 124

RESULT 7

US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-661-052-16

Query Match 81.1%; Score 511.5; DB 2; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNIKDFYMHVWKORPEQGLEWIDPENGSDYA 61
Db 278 IKLQSGAELVSRGTSVKLSCTASGFNIDSYMHVLRQGPQGLEWIDPENGDT 337
QY 62 PKFGKATMTADSSNTAYLQLSLTSETAVYYCN-----AYGDYEGYWGQTTTV 115
Db 338 PKFGKATMTDTSSNTAYLQLSLTSETAVYYCNEGPTGPPYFD---YWGQTTTV 394
QY 116 SS 117
Db 395 SS 396

RESULT 8

US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-188-082-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNIKDFYMHVWKORPEQGLEWIDPENGSDYA 61
Db 278 IKLQSGAELVSRGTSVKLSCTASGFNIDSYMHVLRQGPQGLEWIDPENGDT 337
QY 62 PKFGKATMTADSSNTAYLQLSLTSETAVYYCN-----AYGDYEGYWGQTTTV 115


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; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

Qy 2 VKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSYA 61
Db 278 IKLOQSGAELVRSVTSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDEYA 337

Qy 62 PKFOGKATMTADSSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 115
Db 338 PKFOGKATFTTDTSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 394

Qy 116 SS 117
Db 395 SS 396

RESULT 11
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

Qy 2 VKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSYA 61
Db 278 IKLOQSGAELVRSVTSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDEYA 337

Qy 62 PKFOGKATMTADSSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 115
Db 338 PKFOGKATFTTDTSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 394

Qy 116 SS 117
Db 395 SS 396

RESULT 10
US-09-102-716-16
; Sequence 16, Application US/09102716
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; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

Qy 2 VKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSYA 61
Db 278 IKLOQSGAELVRSVTSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDEYA 337

Qy 62 PKFOGKATMTADSSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 115
Db 338 PKFOGKATFTTDTSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 394

Qy 116 SS 117
Db 395 SS 396

RESULT 11
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

Qy 2 VKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSYA 61
Db 278 IKLOQSGAELVRSVTSVKLSCTASGFNIKDSYMHVLRQGPQGLEWIGWIDPENGDEYA 337

Qy 62 PKFOGKATMTADSSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 115
Db 338 PKFOGKATFTTDTSSNTAYLQLSLTSEDYAVYCN-----AYYGDYEGYWGQTTVTY 394

Qy 116 SS 117
Db 395 SS 396

RESULT 11
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
```

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Duane C. Ulmer
;/ STREET: P.O. Box 1967
;/ CITY: Midland
;/ STATE: MI
;/ COUNTRY: US
;/ ZIP: 48641-1967
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ OPERATING SYSTEM: IBM PC compatible
;/ SOFTWARE: Patent In Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/017,570
;/ FILING DATE: 19930216
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: ULMER, DUANE C
;/ REGISTRATION NUMBER: 34,941
;/ REFERENCE/DOCKET NUMBER: C-38,777
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (517) 636-8104
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 124 amino acids
;/ TYPE: AMINO ACID
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-017-570-4

Query Match 80.3%; Score 506.5; DB 1; Length 124;
Best Local Similarity 76.4%; Pred. No. 2.1e-44;
Matches 97; Conservative 9; Mismatches 8; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNFKDFYHWHVVKORPEQGLEWIGWIDPENGDSY 60
Db 1 EVQLQSGAELVSGASVKMSCTASGFNFKDYHWHVVKORPEQGLEWIGWIDPENGDT 60
QY 61 APRFGKATMTDSSNTAYLQLSLTSEDVAVYCN-----YGDYEGYWGOG 110
Db 61 APRFGKATMTDSSNTAYLQLSLTSEDVAVYCNTRLSTMTITRWFDD---VWGAG 117
QY 111 TTVTVSS 117
Db 118 TTVAVSS 124

RESULT 12
US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/08/471,426
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/017,570
;/ FILING DATE: 16-FEB-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: ULMER, DUANE C
;/ REGISTRATION NUMBER: 34,941
;/ REFERENCE/DOCKET NUMBER: C-38,777
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (517) 636-8104
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 124 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-471-426-4

Query Match 80.3%; Score 506.5; DB 1; Length 124;
Best Local Similarity 76.4%; Pred. No. 2.1e-44;
Matches 97; Conservative 9; Mismatches 8; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNFKDFYHWHVVKORPEQGLEWIGWIDPENGDSY 60
Db 1 EVQLQSGAELVSGASVKMSCTASGFNFKDYHWHVVKORPEQGLEWIGWIDPENGDT 60
QY 61 APRFGKATMTDSSNTAYLQLSLTSEDVAVYCN-----YGDYEGYWGOG 110
Db 61 APRFGKATMTDSSNTAYLQLSLTSEDVAVYCNTRLSTMTITRWFDD---VWGAG 117
QY 111 TTVTVSS 117
Db 118 TTVAVSS 124

RESULT 13
PCT-US94-01709-4
; Sequence 4, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
;/ REFERENCE/DOCKET NUMBER: 38,777-F
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (517) 636-8104
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 124 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 ; Search time 10.8837 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAELVGSASVKL.....AYXDYEGYWGQTTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	631	100.0	117	10	US-09-976-787-23
2	631	100.0	117	10	US-09-865-198-22
3	631	100.0	238	10	US-09-976-787-29
4	631	100.0	238	10	US-09-865-198-28
5	624	98.9	117	10	US-09-976-787-7
6	624	98.9	117	10	US-09-865-198-7
7	624	98.9	240	10	US-09-976-787-28
8	624	98.9	240	10	US-09-865-198-27
9	503.5	79.8	124	9	US-09-974-052-1
10	503.5	79.8	124	9	US-09-974-051-1
11	502.5	79.6	120	10	US-09-910-059-11
12	502.5	79.6	255	10	US-09-910-059-19
13	488.5	77.4	136	10	US-09-564-329A-11
14	488.5	77.4	136	10	US-09-855-153-11
15	488.5	77.4	136	10	US-09-854-811-11
16	488.5	77.4	136	10	US-09-934-773-11
17	488.5	77.4	136	10	US-09-963-620-11
18	478	75.8	117	10	US-09-158-120A-18
19	428.5	67.9	139	10	US-09-809-739-5

20	428	67.8	117	10	US-09-158-120A-17	Sequence 17, Appl
21	422.5	67.0	244	10	US-09-940-391-1	Sequence 1, Appl
22	417.5	66.2	124	9	US-09-974-052-9	Sequence 9, Appl
23	417.5	66.2	124	9	US-09-974-052-12	Sequence 12, Appl
24	417.5	66.2	124	9	US-09-974-051-9	Sequence 9, Appl
25	417.5	66.2	124	9	US-09-974-051-12	Sequence 12, Appl
26	413.5	65.5	124	9	US-09-974-052-8	Sequence 8, Appl
27	413.5	65.5	124	9	US-09-974-051-8	Sequence 8, Appl
28	408.5	64.7	120	10	US-09-910-059-89	Sequence 89, Appl
29	408.5	64.7	120	10	US-09-910-059-79	Sequence 79, Appl
30	407.5	64.6	127	10	US-09-998-831-7	Sequence 7, Appl
31	406.5	64.4	120	10	US-09-910-059-91	Sequence 91, Appl
32	403.5	63.9	120	10	US-09-910-059-85	Sequence 85, Appl
33	402.5	63.8	120	10	US-09-910-059-81	Sequence 81, Appl
34	401.5	63.6	124	9	US-09-974-052-7	Sequence 7, Appl
35	401.5	63.6	124	9	US-09-974-051-7	Sequence 7, Appl
36	401	63.5	138	10	US-09-753-436-78	Sequence 78, Appl
37	400.5	63.5	122	1	US-08-779-784-28	Sequence 28, Appl
38	399.5	63.3	120	10	US-09-910-059-55	Sequence 55, Appl
39	399.5	63.3	153	10	US-09-861-294-4	Sequence 4, Appl
40	399.5	63.3	255	10	US-09-910-059-57	Sequence 57, Appl
41	399.5	63.3	260	10	US-09-910-059-93	Sequence 93, Appl
42	399.5	63.3	306	10	US-09-910-059-95	Sequence 95, Appl
43	399.5	63.3	613	10	US-09-910-059-113	Sequence 113, App
44	399.5	63.3	716	10	US-09-910-059-125	Sequence 125, App
45	398.5	63.2	120	12	US-10-025-687-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-976-787-23

; Sequence 23, Application US/09976787

; Patent No. US20020064528A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

; APPLICANT: Witte, Larry

; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

; FILE REFERENCE: 11245/46505

; CURRENT APPLICATION NUMBER: US/09/976,787

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/493,539

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 23

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Mouse

; US-09-976-787-23

Query Match 100.0%; Score 631; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYHMHVKORPEQGLEWIGWIDPENGSDSY 60

Db 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYHMHVKORPEQGLEWIGWIDPENGSDSY 60

Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGDYEGYWGQTTVTSS 117

Db 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGDYEGYWGQTTVTSS 117

RESULT 2

US-09-865-198-22

; Sequence 22, Application US/09865198

; Patent No. US20020103345A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhenping

```
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match          100.0%; Score 631; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
DB 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
DB 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117

RESULT 3
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match          100.0%; Score 631; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
DB 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
DB 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117

RESULT 4
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
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; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match          100.0%; Score 631; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
DB 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
DB 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117

RESULT 5
US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match          98.9%; Score 624; DB 10; Length 117;
Best Local Similarity 99.1%; Pred. No. 4.7e-42;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
DB 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
DB 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117

RESULT 6
US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
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Query Match
Best Local Similar

[illegible]

THE UNIVERSITY OF CHICAGO

Qy 111 TTVTVSS 117
111 111 111
Db 118 TTVAVSS 124

THE UNIVERSITY OF CHICAGO

APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Harour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
TITLE OF INVENTION: Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974,051
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/029,694
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 124
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: Murine Col-1 VH
LOCATION: 1..124
US-09-974-051-1

Query Match 79.8%; Score 503.5; DB 9; Length 124;
Best Local Similarity 76.4%; Pred. No. 9.5e-33;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;

Qy 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
Db 1 EVQLQSGAELVSRGASVKLSCTASGTFNKNIDYMHVWKQRPQGLEWIGWIDPENGDT 60
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNV-----YGDYEGYWGQ 110
Db 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNVTRGLTTRWTFD---VWGAG 117
Qy 111 TIVTVSS 117
Db 118 TIVAVSS 124

RESULT 11
US-09-910-059-11
Sequence 11, Application US/09910059
Patent No. US20020142359A1
GENERAL INFORMATION:
APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-09-910-059-11

Query Match 79.68%; Score 502.5; DB 10; Length 120;
Best Local Similarity 80.8%; Pred. No. 1.1e-32;
Matches 97; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

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Db 1 EVQLQSGAELVSRGASVKLSCTASGTFNKNIDYMHVWKQRPQGLEWIGWIDPENGDT 60
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNV-----YGDYEGYWGQTTVTVSS 117
Db 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCHVLYAGLYANDYWGQTSVAVSS 120

RESULT 12

US-09-910-059-19
Sequence 19, Application US/09910059
Patent No. US20020142359A1
GENERAL INFORMATION:
APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 255
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimaeric HuIgG2 Fd construct
US-09-910-059-19

Query Match 79.6%; Score 502.5; DB 10; Length 255;
Best Local Similarity 80.8%; Pred. No. 2.1e-32;
Matches 97; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

Qy 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSY 60
Db 20 EVQLQSGAELVSRGASVKLSCTASGTFNKNIDYMHVWKQRPQGLEWIGWIDPENGDT 79
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNV-----YGDYEGYWGQTTVTVSS 117
Db 80 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCHVLYAGLYANDYWGQTSVAVSS 139

RESULT 13

US-09-564-329A-11
Sequence 11, Application US/09564329A
Patent No. US20010055751A1
GENERAL INFORMATION:
APPLICANT: Reiter, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/564,329A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675


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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-11
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Query Match 77.4%; Score 488.5; DB 10; Length 136;
Best Local Similarity 77.8%; Pred. No. 1.5e-31;
Matches 91; Conservative 10; Mismatches 11; Indels 5; Gaps 1;

QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 14 EVQLQSGAELVSRGASVKLSCTASGFNIDYIHVNORPDQGLEWIGWIDPENGDTF 73
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
Db 74 VPKFGKATMTADIFSNATYHLHLSLTSEDYAVYCKT-----GGFWGOGTLVTSSA 125
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RESULT 14
US-09-855-153-11
; Sequence 11, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-11

Query Match 77.4%; Score 488.5; DB 10; Length 136;
Best Local Similarity 77.8%; Pred. No. 1.5e-31;
Matches 91; Conservative 10; Mismatches 11; Indels 5; Gaps 1;

QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 14 EVQLQSGAELVSRGASVKLSCTASGFNIDYIHVNORPDQGLEWIGWIDPENGDTF 73
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
Db 74 VPKFGKATMTADIFSNATYHLHLSLTSEDYAVYCKT-----GGFWGOGTLVTSSA 125
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```
RESULT 15
US-09-854-811-11
; Sequence 11, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-11
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Query Match 77.4%; Score 488.5; DB 10; Length 136;
Best Local Similarity 77.8%; Pred. No. 1.5e-31;
Matches 91; Conservative 10; Mismatches 11; Indels 5; Gaps 1;

QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 14 EVQLQSGAELVSRGASVKLSCTASGFNIDYIHVNORPDQGLEWIGWIDPENGDTF 73
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGDYEGYWGOGTTVTSS 117
Db 74 VPKFGKATMTADIFSNATYHLHLSLTSEDYAVYCKT-----GGFWGOGTLVTSSA 125
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Search completed: December 23, 2002, 07:58:21
Job time : 11.8837 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 23.1279 Seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAELVGSASVKL.....AYGDYGYWGQTTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	81.0	136	2 S04576	Ig heavy chain pre
2	498.5	79.0	268	2 A56446	Ig heavy chain v r
3	486.5	78.7	116	2 S15672	Ig heavy chain v r
4	491	77.8	118	2 S25174	Ig heavy chain v r
5	481.5	76.3	137	2 S52445	Ig heavy chain v r
6	480	76.1	117	2 S17586	Ig heavy chain v r
7	479	75.9	221	2 S49220	Ig gamma-1 chain -
8	476	75.4	120	2 S03471	Ig heavy chain v-D
9	473.5	75.0	178	2 S29594	Ig gamma chain (WM
10	467	74.0	116	2 S24289	Ig gamma chain v r
11	465.5	73.8	114	4 A47271	nitrophenyl phosph
12	461.5	73.1	122	2 S06823	Ig heavy chain v r
13	459	72.7	233	2 JC5322	p53 specific singl
14	455	72.1	120	2 S03484	Ig heavy chain v-D
15	454	71.9	115	2 S03482	Ig heavy chain v-D
16	435	68.9	108	2 PH1012	Ig heavy chain v r
17	433	68.6	249	2 S41374	single chain Fv an
18	430.5	68.2	115	2 PH0246	Ig heavy chain v r
19	430	68.1	123	2 PH1403	Ig heavy chain v r
20	425.5	67.4	107	2 PH1013	Ig heavy chain v r
21	420.5	66.6	118	2 G37267	Ig heavy chain v r
22	416.5	66.0	139	2 PS0024	Ig heavy chain pre
23	410.5	65.1	115	2 A54378	Ig heavy chain v r
24	410	65.0	138	2 S21810	Ig heavy chain v r
25	406.5	64.4	120	2 B22769	Ig gamma chain v r
26	406	64.3	246	2 S38950	Ig gamma chain - m
27	406	64.3	446	2 S40295	Ig gamma-2a chain
28	404.5	64.1	107	2 A27646	Ig heavy chain v r
29	403.5	63.9	116	2 S53751	antibody Fab Jel 1

30	403.5	63.9	139	1 MHMS18	Ig heavy chain pre
31	403.5	63.9	287	4 PC4402	pelB leader/Ig hea
32	400.5	63.5	120	2 S41394	Ig heavy chain v r
33	399.5	63.3	133	2 PC1155	Ig heavy chain pre
34	397.5	63.0	120	2 F28195	Ig heavy chain v r
35	397	62.9	136	2 PL0208	Ig heavy chain pre
36	396	62.8	119	2 D30562	Ig heavy chain v r
37	394.5	62.5	136	2 JL0077	Ig heavy chain pre
38	394.5	62.5	141	2 JL0076	Ig heavy chain pre
39	394.5	62.5	469	2 S37483	Ig gamma-2a chain
40	394	62.4	116	2 S55542	Ig heavy chain v r
41	394	62.4	131	2 A27472	Ig heavy chain pre
42	393.5	62.4	119	2 A24672	Ig heavy chain pre
43	393.5	62.4	120	2 G28195	Ig heavy chain v r
44	393.5	62.4	288	2 S29690	Ig heavy chain vDJ
45	392	62.1	99	2 D37262	Ig heavy chain v r

ALIGNMENTS

RESULT 1

S04576

Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000

C;Accession: S04576

R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;

Eur. J. Immunol. 17, 91-95, 1987

A;Title: Molecular analysis of the murine lupus-associated anti-self response: Involv

A;Reference number: S04573; MUID:87133856; PMID:3102255

A;Accession: S04576

A;Molecule type: mRNA

A;Residues: 1-136 <KOF>

A;Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 511; DB 2; Length 136;

Best Local Similarity 82.9%; Pred. No. 3.7e-39;

Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QVKLQSGAELVGSASVKLSCTTSNGFNKIDFYMHVWKQRPEQGLEWIGWIDPENGUSDY 60

Db 20 EVQLQQSGAELVRPGASVKLSCTASGTFNIDYMHVWKQRPEQGLEWIGWIDPENGSDY 79

Qy 61 AKPFGKATMTADSSNTAYLQLSLTSEDPAVYCYNAYYGDYEGYWGQTTVTVSS 117

Db 80 ASKFGKATMTADTSSNTAYLQLSLTSEDPAVYCYCTYGYAYMDYWGQTSVTVSS 136

RESULT 2

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C;Species: Mus musculus (house mouse)

C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C;Accession: A56446

R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide

A;Reference number: A56446; MUID:95229583; PMID:7713873

A;Accession: A56446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <TAN>

A;Cross-references: GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 79.0%; Score 498.5; DB 2; Length 268;

Best Local Similarity 83.1%; Pred. No. 1e-37;

A:Reference number: A47271; MUID:93165660; PMID:8094556

A:Accession: A47271

A:Molecule type: DNA; protein

A:Residues: 1-134 <LES>

A:Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)

A:Note: parts of this sequence were determined by protein sequencing

F:22-96/Disulfide bonds: #status predicted

Query Match 73.8%; Score 465.5; DB 4; Length 114;

Best Local Similarity 77.8%; Pred. No. 3.9e-35;

Matches 91; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGWIDPENGSDSY 60

Db 1 QVQLQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGRIDPANVDTKY 60

Qy 61 APRFQKATMTADSSNTAYLQSLTSEDYAVYCNAYYDYEGYWGQGTTVTVSS 117

Db 61 DPRFQKATMTADSSNTAYLQSLTSEDYAVYCNAYYDYEGYWGQGTTVTVSS 114

RESULT 12

S06823

Ig heavy chain V region (clone IIC) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: S06823

R:Miller III, A.; Glasel, J.A.

J. Mol. Biol. 209, 763-778, 1989

A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morph

A:Reference number: S06815; MUID:90064531; PMID:2555319

A:Accession: S06823

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-122 <ML>

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:13-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 73.1%; Score 461.5; DB 2; Length 122;

Matches 95; Conservative 8; Mismatches 14; Indels 5; Gaps 3;

Qy 1 QVQLQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGWIDPENGSDS 59

Db 1 EVQLQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGRIDPANVNTK 60

Qy 60 YAPKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYY--GDYEG--YWGQGTTVTV 115

Db 61 YDPKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYY--GDYEG--YWGQGTTVTV 120

Qy 116 SS 117

Db 121 SS 122

RESULT 13

JC5322

p53 specific single-chain antibody Fab421 - human

C:Species: Homo sapiens (man)

C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C:Accession: JC5322

R:Jannot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: JC5322; MUID:97168950; PMID:9016757

A:Accession: JC5322

A:Molecule type: mRNA

A:Residues: 1-233 <JAN>

A:Experimental source: hydrioloma cell

C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match

72.7%; Score 459; DB 2; Length 233;

Best Local Similarity 80.5%; Pred. No. 3.2e-34;

Matches 91; Conservative 5; Mismatches 13; Indels 4; Gaps 1;

Qy 5 QQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGWIDPENGSDYAPKF 64

Db 1 QESGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGRIDPANGDTRSS 60

Qy 65 QKATMTADSSNTAYLQSLTSEDYAVYCNAYYDYEGYWGQGTTVTVSS 117

Db 61 GYKATMTADSSNTAYLQSLTSEDYAVYCNAGM---DYWGQGTTVTVSS 109

RESULT 14

S03484

Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Variety: strain BALB/C

C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000

C:Accession: S03484; S07453

R:Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,

EMBO J. 2, 867-872, 1983

A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-

hypervariable regions

A:Reference number: S03471; MUID:84057768; PMID:6416834

A:Accession: S03484

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 10-120 <ROC1>

A:Cross-references: EMBL:X07144

A:Note: this sequence was determined from the differentiated gene

R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leciercq, L.; Somme, G.; Theze, J.; Foug

J. Immunol. 129, 2554-2558, 1982

A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not

A:Reference number: S07453; MUID:83058021; PMID:6815271

A:Accession: S07453

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-43 <ROC2>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 72.1%; Score 455; DB 2; Length 120;

Matches 90; Conservative 8; Mismatches 19; Indels 2; Gaps 1;

Qy 1 QVQLQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGWIDPENGSDSY 60

Db 1 EVQLQSGAELVSGASVKLSCTTSFNKIDFYMHVWVKRPEQGLEWIGRIDPANXNSKY 60

Qy 61 APKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYY--YGDYEGYWGQGTTVTVSS 117

Db 61 GPKFGKATMTADSSNTAYLQSLTSEDYAVYCNAYY--YGDYEGYWGQGTTVTVSS 119

RESULT 15

S03482

Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Variety: strain BALB/C

C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000

C:Accession: S03482; S07453

R:Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,

EMBO J. 2, 867-872, 1983

A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-

hypervariable regions

A:Reference number: S03471; MUID:84057768; PMID:6416834

A:Accession: S03482

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 10-115 <ROC1>

A:Cross-references: EMBL:X03219

A:Note: this sequence was determined from the differentiated gene

R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leciercq, L.; Somme, G.; Theze, J.; Foug

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 11.564 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAELVSGASVKL.....AYGDYGYWGQTTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	403.5	63.9	139	1	HV07_MOUSE
2	390	61.8	120	1	HV03_MOUSE
3	385.5	61.1	137	1	HV11_MOUSE
4	381	60.4	140	1	HV02_MOUSE
5	377	59.7	117	1	HV12_MOUSE
6	374	59.3	138	1	HV48_MOUSE
7	368	58.3	117	1	HV13_MOUSE
8	368	58.3	136	1	HV15_MOUSE
9	366.5	58.1	120	1	HV50_MOUSE
10	364.5	57.8	147	1	HV1C_HUMAN
11	362.5	57.4	118	1	HV51_MOUSE
12	348	55.2	121	1	HV01_MOUSE
13	345	54.7	117	1	HV06_MOUSE
14	343	54.4	117	1	HV09_MOUSE
15	339	53.7	117	1	HV04_MOUSE
16	336	53.2	117	1	HV49_MOUSE
17	332	52.6	117	1	HV10_MOUSE
18	332	52.6	117	1	HV52_MOUSE
19	327	51.8	117	1	HV1B_HUMAN
20	325	51.5	117	1	HV05_MOUSE
21	323.5	51.3	119	1	HV40_MOUSE
22	321.5	51.0	119	1	HV37_MOUSE
23	320	50.7	117	1	HV14_MOUSE
24	316.5	50.2	114	1	HV00_MOUSE
25	314.5	49.8	119	1	HV38_MOUSE
26	312	49.4	117	1	HV42_MOUSE
27	309	49.0	117	1	HV1G_HUMAN
28	308.5	48.9	136	1	HV16_MOUSE
29	307.5	48.7	122	1	HV3G_HUMAN
30	305	48.3	142	1	HV01_RAT
31	303	48.0	117	1	HV1A_HUMAN
32	296	46.9	118	1	HV39_MOUSE
33	293.5	46.5	122	1	HV21_MOUSE

Query Match 63.9%; Score 403.5; DB 1; Length 139;
Best Local Similarity 65.8%; Pred. No. 2.4e-33;

ALIGNMENTS

RESULT 1

ID	HV07_MOUSE	STANDARD;	PRT;	139 AA.
AC	P01751; P01752;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region B1-8/186-2 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;			
RX	MEDLINE=81234548; PubMed=6788376;			
RA	Bothwell A.B.M.; Faskind M.; Rech M.; Imanishi-Kari T.; Rajewsky K.;			
RA	Baltimore D.;			
RT	"Heavy chain variable region contribution to the Npb family of			
RT	antibodies: somatic mutation evident in a gamma 2a variable region.";			
RL	Cell 24:625-637(1981).			
CC	-I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA			
CC	MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL			
CC	(NPB ANTIBODIES).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: J00529; AAA38170.1; -			
DR	PIR: A02034; MHMS18.			
DR	HSSP; P01810; 2FBJ.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; ig; 1.			
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KW	Immunoglobulin v region; Signal.			
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FT	CHAIN 20 139			
FT	DOMAIN 20 49			
FT	DOMAIN 50 54			
FT	DOMAIN 55 68			
FT	DOMAIN 69 85			
FT	DOMAIN 86 117			
FT	DOMAIN 118 124			
FT	DOMAIN 125 139			
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P01781 homo sapien
P01800 mus musculu
P01796 mus musculu
P01802 mus musculu
P01762 homo sapien

117 1 HV41_MOUSE
123 1 HV24_MOUSE
113 1 HV30_MOUSE
115 1 HV32_MOUSE
125 1 HV1F_HUMAN
119 1 HV3L_HUMAN
123 1 HV19_MOUSE
116 1 HV3T_HUMAN
113 1 HV31_MOUSE
113 1 HV27_MOUSE
115 1 HV33_MOUSE
122 1 HV3A_HUMAN

293 46.4
291 46.1
290 46.0
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289 45.8
287 45.5
286.5 45.4
286 45.3
285 45.2
284 45.0
283.5 44.9

34 293
35 291
36 290
37 290
38 290
39 289
40 287
41 286.5
42 286
43 285
44 284
45 283.5

```
Matches 79; Conservative 13; Mismatches 25; Indels 3; Gaps 2;

QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGSDSY 60
Db 20 QVLOQSGAELVSGASVKLSCKASGYTFTSYMHVWKQRPQGRGLEWIGRIDPNSGGTKY 79
QY 61 APKFOGKATMTADSSNTAYLQLSLTSSTEDTAVYYCNA--YYG-DYEGYWGQTTVTVSS 117
Db 80 NEHFKSKATLTIDKPSSTAYMQLSLTSDSAVYYCARYLGRYFDYWGQTTLTVSS 139

RESULT 2
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE. THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVMSG7.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER# 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 61.8%; Score 390; DB 1; Length 120;
Best Local Similarity 62.5%; Pred. No. 4.4e-32;
Matches 75; Conservative 19; Mismatches 22; Indels 4; Gaps 2;

QY 2 VKEQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGSDYA 61
Db 1 VQLOQSGAELVSGASVKLSCKASGYTFTSYGINVWKQRPQGLEWIGYINPGYTKYN 60
QY 62 PKFGKATMTADSSNTAYLQLSLTSSTEDTAVYYC--NAYGD--YEGYWGQTTVTVSS 117
Db 61 EKFKGKTTLVDRKSSSTAYMQLSLTSDSAVYYCARYLGRYFDYWGQTTLTVSS 120

RESULT 3
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
```

```
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 61.1%; Score 385.5; DB 1; Length 137;
Best Local Similarity 63.6%; Pred. No. 1.4e-31;
Matches 75; Conservative 12; Mismatches 30; Indels 1; Gaps 1;

QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGSDSY 60
Db 20 QVLOQSGAELVSGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79
QY 61 APKFOGKATMTADSSNTAYLQLSLTSSTEDTAVYYCNA--YGDYEGYWGQTTVTVSS 117
Db 80 NEHFKSKATLTIDKPSSTAYMQLSLTSDSAVYYCARYLGRYFDYWGQTTLTVSS 137

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC
```


DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Cleveland B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A26262; MMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
Query Match 58.3%; Score 368; DB 1; Length 117;
Best Local Similarity 61.3%; Pred. No. 6.5e-30;
Matches 7; Conservative 16; Mismatches 26; Indels 4; Gaps 2;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWQKRPQGLEWIGWIDPENGSDY 60
DB 1 EVQLQSGPELVKPGASVKMSCKASGVTFTDYMKWKQSHGKSLWIGDINPNNGTST 60
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYWGQGTITVTVSS 117
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYCYCARDRYW--YFDVWGAGTTTVTVSS 117
RESULT 8
HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -----
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CC -----
DR EMBL: J00494; AAA38130.1;
DR PIR: A02042; HVMSB1.
DR HSSP; P01772; 2FB4.

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
Query Match 58.3%; Score 368; DB 1; Length 136;
Best Local Similarity 59.0%; Pred. No. 7.7e-30;
Matches 69; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWQKRPQGLEWIGWIDPENGSDY 60
DB 20 QVQLQSGPEVPRGVSVKISCKGSGTFTDYAMHWVQSHAKSLEWIGVISYNGTSTY 79
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYWGQGTITVTVSS 117
DB 80 NQKFKGKATMTVDKSSSTVHMLARLTSEDSANLYCARYYGNFYDWGQGTITVTVSS 136
RESULT 9
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 105
FT DOMAIN 106 120
FT DISULFID 22 96
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 914453F426F09834 CRC64;
Query Match 58.1%; Score 366.5; DB 1; Length 120;
Best Local Similarity 58.2%; Pred. No. 9.4e-30;
Matches 71; Conservative 16; Mismatches 28; Indels 7; Gaps 2;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWQKRPQGLEWIGWIDPENGSDY 60
DB 1 QVQLQSGTELKPGASVNLSCASGVTFTSYMHVWIRQRPQGLEWIGVISNGGTNY 60
QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYEG-----YWGQGTITVTV 115
DB 61 NEKFKSKATLTVDKSSSATYMLSTPTSEDSAVYICARW--DYEGRYFDVWGTTTTVTV 118
QY 116 SS 117
DB 119 SS 120

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RESULT 10
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR: A02046; EIHUND.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 57.8%; Score 364.5; DB 1; Length 147;
Best Local Similarity 51.6%; Pred. No. 1.9e-29;
Matches 66; Conservative 25; Mismatches 26; Indels 11; Gaps 2;

QY 1 QVKLOQSGAELVGSGAVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
DB 20 Q7QLVQSGAEVRKPGASVRSKASGYTFIDSYIHWIRQAPGHGLEWGWINPNSSGGTNY 79
QY 61 APKFGKATMTADSSNTAYLQSLTSDTAVYVC---NAYIGYEGY-----WQO 109
DB 80 APFQGRVMTDRDSFSTAYNDLSRLSDSDSAVFCANSDPFWSDYFNFDYSITLDVRGQ 139
QY 110 GTTVTVSS 117
DB 140 GTTVTVSS 147

RESULT 11
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 57.4%; Score 362.5; DB 1; Length 118;
Best Local Similarity 59.7%; Pred. No. 2.3e-29;
Matches 71; Conservative 17; Mismatches 28; Indels 3; Gaps 2;

QY 1 QVKLOQSGAELVGSGAVKLSCTTSGFNKIDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
DB 1 EVQLQSGPELVKPGASVKISKASGYTFIDYIMNWKQSHGKSLWIGDINPNNGGTSY 60
QY 61 APKFGKATMTADSSNTAYLQSLTSDTAVYVCNAYIGYEGY--WGQGTFTTVVSS 117
DB 61 NQKFRGKATLVDKSSATYMEIRLTSDSAVYICARGYG-YDFPDWGTGTTTVVSS 118

RESULT 12
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR: A02027; GVMS11.
DR HSSP; P01810; 2FRJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 55.2%; Score 348; DB 1; Length 121;
Best Local Similarity 56.2%; Pred. No. 6.6e-28;
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DR PIR: A02030; HVMS23.
DR HSP: P01810; 2PBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 53.7%; Score 339; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 4.9e-27;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYHWHVKQRPEQGLEWIGWIDPENGDSY 60
Db 20 QVQLQPGTGLVKGASVKLSCKASGYFTSYWHWHVKQRPGQGLEWIGNINPGNGTNY 79

Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYC 96
Db 80 NEKPKSKVTLTVDKSSSTAYTQLSLTSEDSAVYC 115

Search completed: December 23, 2002, 07:26:13
Job time : 11.564 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 48.5233 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAELVSGASVKL.....AYYGDYEGYWGQGTIVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_21.*
- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-virus.*
- 16: sp-bacteriap.*
- 17: sp-archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	510	80.8	468	11 Q99L31	Q99L31 mus musculus
2	428	67.8	109	11 Q9JL85	Q9JL85 mus musculus
3	411.5	65.2	143	11 Q924P9	Q924P9 mus musculus
4	407	64.5	146	11 Q924R8	Q924R8 mus musculus
5	403.5	63.9	145	11 Q924Q7	Q924Q7 mus musculus
6	403	63.9	145	11 Q924Q3	Q924Q3 mus musculus
7	400.5	63.5	118	11 Q92IC4	Q92IC4 mus musculus
8	400.5	63.5	473	11 Q99L25	Q99L25 mus musculus
9	399	63.2	473	11 Q99L25	Q99L25 mus musculus
10	398.5	63.2	143	11 Q9D8L4	Q9D8L4 mus musculus
11	398.5	63.2	143	11 Q924R0	Q924R0 mus musculus
12	398	63.1	140	11 Q924R2	Q924R2 mus musculus
13	397	62.9	142	11 Q924Q1	Q924Q1 mus musculus
14	395.5	62.7	145	11 Q924R4	Q924R4 mus musculus
15	394.5	62.5	145	11 Q924R1	Q924R1 mus musculus
16	394	62.4	142	11 Q924Q2	Q924Q2 mus musculus

17	391.5	62.0	143	11 Q91V67	Q91V67 mus musculus
18	391.5	62.0	145	11 Q924Q9	Q924Q9 mus musculus
19	391	62.0	144	11 Q924P5	Q924P5 mus musculus
20	390.5	61.9	137	11 Q924R6	Q924R6 mus musculus
21	390.5	61.9	145	11 Q924Q6	Q924Q6 mus musculus
22	389.5	61.7	143	11 Q924P6	Q924P6 mus musculus
23	387.5	61.4	143	11 Q924R7	Q924R7 mus musculus
24	387	61.3	140	11 Q924P8	Q924P8 mus musculus
25	387	61.3	481	11 Q91WT1	Q91WT1 mus musculus
26	386.5	61.3	141	11 Q924Q4	Q924Q4 mus musculus
27	386.5	61.3	145	11 Q924P7	Q924P7 mus musculus
28	385.5	61.1	145	11 Q924R3	Q924R3 mus musculus
29	383.5	60.8	139	11 Q924R5	Q924R5 mus musculus
30	382.5	60.6	143	11 Q91VA2	Q91VA2 mus musculus
31	381	60.4	117	11 Q9QXF0	Q9QXF0 mus musculus
32	380	60.2	489	11 Q8VCX4	Q8VCX4 mus musculus
33	379.5	60.1	278	11 Q921K1	Q921K1 mus musculus
34	379.5	60.1	613	11 Q8VCX7	Q8VCX7 mus musculus
35	377	59.7	117	11 Q9QXE9	Q9QXE9 mus musculus
36	376	59.6	146	11 Q924Q8	Q924Q8 mus musculus
37	375	59.4	168	11 Q8VDC9	Q8VDC9 mus musculus
38	374	59.3	474	11 Q8R3H6	Q8R3H6 mus musculus
39	373.5	59.2	143	11 Q924Q0	Q924Q0 mus musculus
40	372	59.0	147	11 Q925S3	Q925S3 mus musculus
41	370.5	58.7	109	11 Q9JL75	Q9JL75 mus musculus
42	368	58.3	170	11 Q925S2	Q925S2 mus musculus
43	367	58.2	481	11 Q91WT3	Q91WT3 mus musculus
44	363.5	57.6	463	11 Q99L24	Q99L24 mus musculus
45	362.5	57.4	124	4 Q9UL92	Q9UL92 homo sapien

ALIGNMENTS

RESULT 1

- Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
- AC Q99L31:
- DT 01-JUN-2001 (TREMREL. 17, Created)
- DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
- DE 01-JUN-2002 (TREMREL. 21, Last annotation update)
- DE Similar to RIKEN cDNA 1810060009 gene.
- OS Mus musculus (Mouse).
- OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
- OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
- OX NCBI_taxid=10090;
- RN [1]
- RP SEQUENCE FROM N.A.
- RA Strausberg R.;
- RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
- DR EMBL; BC003878; AAH03878.1; -.
- DR HSSP; P01842; 7FAB.
- DR InterPro; IPR003599; Ig.
- DR InterPro; IPR003597; Ig_c1.
- DR InterPro; IPR003600; Ig_like.
- DR InterPro; IPR003006; Ig_MHC.
- DR InterPro; IPR003596; Ig_v.
- DR Pfam; PF00047; Ig; 3.
- DR SMART; SM00409; IG; 2.
- DR SMART; SM00407; IGC1; 3.
- DR SMART; SM00406; IGV; 1.
- DR SMART; SM00410; IG_like; 1.
- DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
- SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 80.8%; Score 510; DB 11; Length 468;

Best Local Similarity 80.7%; Pred. No. 1.3e-44;

Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDPYMHVQRPQGLEWIGWIDPENGSDSDY 60

Db 20 EVQLQSGAELVRPGASVKLSCTASGFKSLMHWVQRPQGLEWIGWIDPENGSDSDY 79

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067793; BAB63278.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 63.9%; Score 403.5; DB 11; Length 145;
Best Local Similarity 65.8%; Pred. No. 3.4e-34;
Matches 79; Conservative 13; Mismatches 25; Indels 3; Gaps 2;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKORPQGLEWIGWIDPENGDSY 60
DB 1 QVLOQPGALVKPKASVKLSKASGYFTFSYMHVWVKORPQGLEWIGRIDPNSGGTY 60

QY 61 APKFOGKATMTADSSNTAYLQSLTSSEDTAVYYCNA--YYG-DYEGYWGQGTITVTVSS 117
DB 61 NEKFSKATLTVDKPSSTAYMQLSLSLTSSEDSAVYYCARYDYIGSSYFDYWGQGTITVTVSS 120

RESULT 6
QY24Q3
ID Q924Q3 PRELIMINARY; PRT; 146 AA.
AC Q924Q3;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE VH186.2-D-J-c mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067797; BAB63282.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 63.9%; Score 403; DB 11; Length 146;
Best Local Similarity 66.1%; Pred. No. 3.9e-34;
Matches 80; Conservative 14; Mismatches 23; Indels 4; Gaps 3;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKORPQGLEWIGWIDPENGDSY 60
DB 1 QVLOQPGALVKPKASVKLSKASGYFTFSYMHVWVKORPQGLEWIGRIDPNSGGTY 60

QY 61 APKFOGKATMTADSSNTAYLQSLTSSEDTAVYYC--NAY-YGDYE-GYWGQGTITVTVS 116
DB 61 NEKFSKATLTVDKPSSTAYMQLSLSLTSSEDSAVYYCARSLYDGYDAMDYWGQGTITVTVS 120

QY 117 S 117
DB 121 S 121
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RESULT 7
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ID Q921C4 PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U78801; AAD00293.1; -.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EC59D31EC4FC CRC64;

Query Match 63.5%; Score 400.5; DB 11; Length 118;
Best Local Similarity 66.1%; Pred. No. 5.5e-34;
Matches 78; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKORPQGLEWIGWIDPENGDSY 60
DB 1 QVQVQSGAELARPWASVKLSKASGYNSYMWQVWVKORPQGLEWIGAIYPGQDTSY 60

QY 61 APKFOGKATMTADSSNTAYLQSLTSSEDTAVYYC--NAYYGDYEGYWGQGTITVTVSS 117
DB 61 TQFRGKATLTADKSSSTAYMQLSLSSEDSAVYYCARTVGGYFDYWGQGTITVTVSS 118

RESULT 8
QY9L25
ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003888; AA03888.1; -.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003597; Ig.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_Like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
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Best Local Similarity	64.7%;	Pred. No. 4.3e-33;	Matches 77;	Conservative 18;	Mismatches 22;	Indels 2;	Gaps 1;
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Db	20	QVQLKQSGAELVKPGASVKISCKASGYTDDYINNVKQRPQGLEWIGKIPGSGSTYY 79					
QY	61	APKFGKATMTADSSNTAYLQLSLTSEDYAVYIC--NAYYGDYEGYWGQGTVTTVSS 117					
Db	80	NEKFKSKATLTADKSSSTAYMQLSLTSEDSAVYFCARSGYDYDWFAYWGQGTTLTVSA 138					
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ID	Q924R0	PRELIMINARY;					143 AA.
AC	Q924R0;						
DT	01-DEC-2001 (TREMBLrel. 19, Created)						
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)						
DT	01-WAR-2002 (TREMBLrel. 20, Last annotation update)						
DE	VH186.2-D-J-C mu protein (Fragment).						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
NCBI_TaxID=10090;							
OX	NCBI_TaxID=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=C57BL/6;						
RA	Kozono Y., Kozono H., Azuma T.;						
RT	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals						
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-						
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP).";						
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AB067790; BAB63275.1;						
DR	InterPro; IPR003598; Ig_C2.						
DR	InterPro; IPR003006; Ig_MHC.						
DR	Pfam; PF00047; Ig.1.						
DR	SMART; SM00408; Igc2; 1.						
DR	Immunoglobulin domain.						
FT	NON_TER 1						
FT	NON_TER 143						
SEQ	SEQUENCE 143 AA; 15868 MW; 13982E966B81E07F CRC64;						
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Best Local Similarity 65.3%; Pred. No. 1.1e-33;							
Matches 77; Conservative 14; Mismatches 26; Indels 1; Gaps 1;							
QY	1	QVKLOQSGAELVCGASVKLSCTTSCFNLIKDFYMHVWKORPQGLEWIGWIDPENGDSY 60					
Db	1	QVQLKQSGAELVKPGASVKLSCKASGYTDDYINNVKQRPQGLEWIGRIDPNSGGTKY 60					
QY	61	APKFGKATMTADSSNTAYLQLSLTSEDYAVYIC--NAYYGDYEGYWGQGTVTTVSS 117					
Db	61	NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYFCARWDEYANDYWGQGTSLTVSS 118					
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Q924Q5		PRELIMINARY;					
ID	Q924Q5	PRELIMINARY;					143 AA.
AC	Q924Q5;						
DT	01-DEC-2001 (TREMBLrel. 19, Created)						
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)						
DT	01-WAR-2002 (TREMBLrel. 20, Last annotation update)						
DE	VH186.2-D-J-C mu protein (Fragment).						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
NCBI_TaxID=10090;							
OX	NCBI_TaxID=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=C57BL/6;						
RA	Kozono Y., Kozono H., Azuma T.;						

RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-


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AC Q924RL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VHI86.2-D30-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067789; BAB63274.1; -.
DR InterPro:IPR03006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
ET NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match: 62.5%; Score 394.5; DB 11; Length 145;
Best Local Similarity 64.2%; Pred. No. 3e-33;
Matches 77; Conservative 13; Mismatches 27; Indels 3; Gaps 1;

Qy 1 QVKGQSGAELVGSVKLSCTTSGFNKDFYMHVVKRPEQGLEWIGWIDPENGSDSY 60
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Db 1 QVKGQSGAELVKSCKASGYTFTSYMHVVKRPEQGLEWIGRIDPNSGGTKY 60
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Qy 61 APKSGKATWTADSSNTAYLQLSLTSEDYAVYCNAYYGD---YEGYWGQGTFTVYSS 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 NEKPKKATLTVDKPSSTAYMQLSLTSEDSAVYCYARYDGSFYMADYWGQGTFTVYSS 120
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Search completed: December 23, 2002, 07:29:59
Job time : 49.5233 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 19.1047 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-23

Perfect score: 549

Sequence: 1 DIELTQSPAIMSASPGKVT.....CQORSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534	97.3	235	4	US-09-171-945-17
2	532	96.9	108	4	US-09-171-945-9
3	529	96.4	129	2	US-08-116-778E-2
4	529	96.4	129	2	US-08-438-562-2
5	529	96.4	129	2	US-08-483-528B-92
6	523	95.3	270	2	US-08-652-507-2
7	523	95.3	553	2	US-08-661-052-16
8	523	95.3	553	4	US-08-188-082-16
9	523	95.3	553	4	US-09-364-088-16
10	523	95.3	553	4	US-09-102-716-16
11	521	94.9	281	4	US-09-423-439-44
12	521	94.9	666	4	US-09-423-439-51
13	518	94.4	105	3	US-08-434-000A-12
14	518	94.4	105	4	US-09-312-157-12
15	516	94.0	106	1	US-07-634-278-1
16	516	94.0	106	1	US-07-634-278-16
17	516	94.0	106	1	US-08-477-728-1
18	516	94.0	106	1	US-08-477-728-16
19	516	94.0	106	1	US-08-474-040-1
20	516	94.0	106	1	US-08-474-040-16
21	516	94.0	106	1	US-08-487-200-1
22	516	94.0	106	1	US-08-487-200-16
23	516	94.0	106	1	US-08-488-113B-163
24	516	94.0	106	1	US-08-477-484B-163
25	516	94.0	106	1	US-08-107-669D-49
26	516	94.0	106	1	US-08-472-788A-83
27	516	94.0	106	2	US-08-477-531B-49

28 516 94.0 106 2 US-08-646-360-163 Sequence 163, App
29 516 94.0 106 2 US-08-082-842A-83 Sequence 83, Appl
30 516 94.0 106 4 US-08-839-765-163 Sequence 163, App
31 516 94.0 106 4 US-09-136-389-163 Sequence 163, App
32 516 94.0 106 4 US-08-484-537-1 Sequence 1, Appl
33 516 94.0 106 4 US-08-484-537-16 Sequence 16, Appl
34 516 94.0 106 4 US-09-610-838-163 Sequence 163, App
35 516 94.0 239 3 US-08-279-772A-8 Sequence 8, Appl
36 516 94.0 239 4 US-08-902-486-11 Sequence 11, Appl
37 516 94.0 599 1 US-08-463-163-3 Sequence 3, Appl
38 493 89.8 130 4 US-09-393-385B-113 Sequence 113, App
39 490 89.3 130 4 US-09-393-385B-111 Sequence 111, App
40 489 89.1 128 4 US-08-619-491-2 Sequence 2, Appl
41 489 89.1 128 5 PCT-US95-07302-2 Sequence 2, Appl
42 483 88.0 244 2 US-08-553-497A-20 Sequence 20, Appl
43 481 87.6 107 1 US-08-211-202-3 Sequence 3, Appl
44 481 87.6 246 1 US-08-469-486-57 Sequence 57, Appl
45 481 87.6 246 2 US-08-469-658-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1

US-09-171-945-17
; Sequence 17, Application US/09171945
; Patent No. 6277599

GENERAL INFORMATION:
; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171.945

; CURRENT FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: GB9703103.3

; PRIOR FILING DATE: 1997-02-14

; PRIOR APPLICATION NUMBER: GB9609405.7

; PRIOR FILING DATE: 1996-05-04

; PRIOR APPLICATION NUMBER: PCT/GB97/01165

; PRIOR FILING DATE: 1997-04-29

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-17

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Best Local Similarity 96.2%; Pred. No. 1.7e-40;

Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 23 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFOQKPGTSPKLIWSTSNLASSVPAR 82

Oy 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106

Db 83 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 128

RESULT 2

US-09-171-945-9

; Sequence 9, Application US/09171945

; Patent No. 6277599

GENERAL INFORMATION:

; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham

; APPLICANT: Edge, Michael Derek

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; US-08-116-778E-2

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Best Local Similarity 97.1%; Pred. No. 2.5e-40;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0

QY 2 IELTQSPAINASPGKVTITTCSSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPA
Db 24 IVLTQSPAINASPGKVTITTCSSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPA
QY 62 SSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 84 SSGSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 128

RESULT 4
US-08-438-562-2
; Sequence 2, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNAWA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95

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/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/116,778
/ FILING DATE: 07-SEP-93
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WILSON, MARY J.
/ REGISTRATION NUMBER: 32,955
/ REFERENCE/DOCKET NUMBER: 249-76
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)816-4000
/ TELEFAX: (703)816-4100
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 129 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: -22..-1
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
/ FEATURE:
/ NAME/KEY: domain
/ LOCATION: 24..33
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
/ FEATURE:
/ NAME/KEY: domain
/ LOCATION: 49..55
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
/ US-08-438-562-2
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/ Query Match 96.4%; Score 529; DB 2; Length 129;
/ Best Local Similarity 97.1%; Pred. No. 2.5e-40;
/ Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARF 61
/ Db 24 IVLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARF 83
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/ QY 62 SGSGSGTYSYSLTISRMEADAATYTCQORSYPYTFGGTKLEIK 106
/ Db 84 SGSGSGTYSYSLTISRMEADAATYTCQORSYPYTFGGTKLEIK 128
/
/ RESULT 5
/ US-08-483-528B-92
/ Sequence 92, Application US/08483528B
/ Patent No. 5939532
/ GENERAL INFORMATION:
/ APPLICANT: NAKAMURA, KAZUYASU
/ APPLICANT: KOIKE, MASAMICHI
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: KURANA, YOSHITHISA
/ APPLICANT: HASEGAWA, MAMORU
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ NUMBER OF SEQUENCES: 103
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/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON & VANDERHYE P.C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: U.S.A.
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/483,528B
/ FILING DATE: 07-JUN-95
/ CLASSIFICATION: 536
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)816-4000
/ TELEFAX: (703)816-4100
/ INFORMATION FOR SEQ ID NO: 92:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 129 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: -22..-1
/ IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
/ IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
/ FEATURE:
/ NAME/KEY: domain
/ LOCATION: 24..33
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
/ FEATURE:
/ NAME/KEY: domain
/ LOCATION: 49..55
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
/ US-08-483-528B-92
/
/ Query Match 96.4%; Score 529; DB 2; Length 129;
/ Best Local Similarity 97.1%; Pred. No. 2.5e-40;
/ Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARF 61
/ Db 24 IVLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARF 83
/
/ QY 62 SGSGSGTYSYSLTISRMEADAATYTCQORSYPYTFGGTKLEIK 106
/ Db 84 SGSGSGTYSYSLTISRMEADAATYTCQORSYPYTFGGTKLEIK 128
/
/ RESULT 6
/ US-08-652-507-2
/ Sequence 2, Application US/08652507
/ Patent No. 5876691
/ GENERAL INFORMATION:
/ APPLICANT:
```

;; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
;; TITLE OF INVENTION:
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon & Vanderhye, P.C.
;; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 2201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/652,507
;; FILING DATE: 02-Jul-1996
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Arthur R. Crawford
;; REGISTRATION NUMBER: 25,327
;; REFERENCE/DOCKET NUMBER: 117-211
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-816-4000
;; TELEFAX: 703-816-4100
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 270 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-652-507-2

Query Match 95.3%; Score 523; DB 2; Length 270;
Best Local Similarity 97.1%; Pred. No. 1.9e-39;
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 LTQSPAIMSASPEKVTITCSASSSYVMHWFQKPGTSPKLIWYSTSLASGVPARFSG 63
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DB 165 LTQSPAIMSASPEKVTITCSASSSYVMHWFQKPGTSPKLIWYSTSLASGVPARFSG 224
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QY 64 SSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 106
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DB 225 SSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 267
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RESULT 7
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052

;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/484,172
;; FILING DATE: 07-JUNE-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Arnold, Beth E.
;; REGISTRATION NUMBER: MXI-043CP
;; REFERENCE/DOCKET NUMBER: MXI-043CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-5941
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 553 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-661-052-16
Query Match 95.3%; Score 523; DB 2; Length 553;
Best Local Similarity 97.1%; Pred. No. 4e-39;
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 LTQSPAIMSASPEKVTITCSASSSYVMHWFQKPGTSPKLIWYSTSLASGVPARFSG 63
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DB 415 LTQSPAIMSASPEKVTITCSASSSYVMHWFQKPGTSPKLIWYSTSLASGVPARFSG 474
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QY 64 SSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 106
|||||
DB 475 SSGSGTSYSLTISRMEADAATYTCQORSSYPFTFGSGTKLEIK 517
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RESULT 8
US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid

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Db	415	LTQSPATMSAPGKPKVITTCSSASSVSVMHWFQOKP	474	LTQSPATMSAPGKPKVITTCSSASSVSVMHWFQOKP	474
QY	64	SGSGTSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK	106	SGSGTSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK	106
Db	475	SGSGTSLTISRMEADAATYYCQRRSSYPFTFGAGTKLEIK	517	SGSGTSLTISRMEADAATYYCQRRSSYPFTFGAGTKLEIK	517

NUMBER OF COPIES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.

Best Local Similarity 93.3%; Pred. No. 1.9e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 60
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Db 1 DIVMTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 60
|| :|||||
QY 61 FSGSGGTSYSLTISRMEADAATYTCOORSSYPFTFGSGTKLEI 105
|||||
Db 61 FSGSGGTSYSLTISRMEADAATYTCOORSSYPFTFGSGTKLEI 105
|||||

RESULT 14

US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351

SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: Guy's 13 kappa
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-312-157-12
Query Match 94.4%; Score 518; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 1.9e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 60
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Db 1 DIVMTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 60
|| :|||||
QY 61 FSGSGGTSYSLTISRMEADAATYTCOORSSYPFTFGSGTKLEI 105
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Db 61 FSGSGGTSYSLTISRMEADAATYTCOORSSYPFTFGSGTKLEI 105
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RESULT 15

US-07-634-278-1
; Sequence 1, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..106
; OTHER INFORMATION: /note= "Variable region of the mouse
; OTHER INFORMATION: anti-Tac antibody light chain."
US-07-634-278-1

Query Match 94.0%; Score 516; DB 1; Length 106;
Best Local Similarity 93.3%; Pred. No. 2.9e-39;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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|| :|||||
Db 2 IVLTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPARF 61
|| :|||||
QY 62 SGSGSGTSYSLTISRMEADAATYTCOORSSYPFTFGSGTKLEIK 106
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Db 62 SGSGSGTSYSLTISRMEADAATYTCOORSSYPFTFGSGTKLEIK 106
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Job time : 20.1047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-865-198-23

Perfect score: 549

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Minimum DB seq length: 0

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	549	100.0	108	10	US-09-865-198-8
5	549	100.0	238	10	US-09-976-787-29
6	549	100.0	238	10	US-09-865-198-28
7	549	100.0	240	10	US-09-976-787-28
8	549	100.0	240	10	US-09-865-198-27
9	534	97.3	235	10	US-09-910-059-17
10	532	96.9	108	10	US-09-910-059-9
11	518	94.4	105	9	US-09-982-107-12
12	518	94.4	669	9	US-09-807-721-2
13	509	92.7	107	9	US-09-144-886-88
14	506	92.2	119	10	US-09-808-037-28
15	506	92.2	239	10	US-09-808-037-6
16	500	91.1	107	9	US-09-144-886-76
17	495	90.2	107	9	US-09-144-886-90
18	484	88.2	107	9	US-09-144-886-75
19	484	88.2	107	9	US-09-144-886-78

20	479	87.2	107	9	US-09-144-886-82	Sequence 82, Appl
21	479	87.2	107	9	US-09-144-886-83	Sequence 83, Appl
22	479	87.2	109	9	US-09-144-886-91	Sequence 91, Appl
23	478	87.1	131	10	US-09-881-823-6	Sequence 6, Appl
24	475.5	86.6	112	9	US-09-144-886-89	Sequence 89, Appl
25	466	84.9	109	9	US-09-144-886-96	Sequence 96, Appl
26	463	84.3	106	10	US-09-158-120A-35	Sequence 35, Appl
27	461	84.0	106	10	US-09-965-099-105	Sequence 105, App
28	461	84.0	106	12	US-10-051-852-105	Sequence 105, App
29	461	84.0	107	10	US-09-965-099-11	Sequence 11, Appl
30	461	84.0	107	12	US-10-051-852-11	Sequence 11, Appl
31	461	84.0	109	9	US-09-144-886-79	Sequence 79, Appl
32	461	84.0	112	10	US-09-965-099-103	Sequence 103, App
33	461	84.0	112	12	US-10-051-852-103	Sequence 103, App
34	460	83.8	109	9	US-09-144-886-97	Sequence 97, Appl
35	454	82.7	109	9	US-09-144-886-77	Sequence 77, Appl
36	454	82.7	109	9	US-09-144-886-98	Sequence 98, Appl
37	453	82.5	107	10	US-09-910-059-71	Sequence 71, Appl
38	453	82.5	235	10	US-09-910-059-99	Sequence 99, Appl
39	449	81.8	127	10	US-09-753-436-80	Sequence 80, Appl
40	448	81.6	106	10	US-09-893-615-89	Sequence 89, Appl
41	442	80.5	107	10	US-09-910-059-61	Sequence 61, Appl
42	440	80.1	107	10	US-09-910-059-50	Sequence 50, Appl
43	440	80.1	235	10	US-09-910-059-52	Sequence 52, Appl
44	437	79.6	109	9	US-09-144-886-92	Sequence 92, Appl
45	432	78.7	107	10	US-09-910-059-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
; US-09-976-787-24

Query Match	100.0%;	Score 549;	DB 10;	Length 106;
Best Local Similarity	100.0%;	Pred. No. 5 3e-31;		
Matches 106;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DIELTQSPAINASPGKVTITCSASSVSVMHFMFQKPGTSPKLIWYSTNLASGVAPAR	60	
Db	1	DIELTQSPAINASPGKVTITCSASSVSVMHFMFQKPGTSPKLIWYSTNLASGVAPAR	60	
Qy	61	FSGSGSGTYSILTISRMAEDAAATYYCQORSSYPFTFGSGTKLEIK	106	
Db	61	FSGSGSGTYSILTISRMAEDAAATYYCQORSSYPFTFGSGTKLEIK	106	

RESULT 2
US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping

```
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US 09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match      100.0%; Score 549; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.3e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 3
US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8

Query Match      100.0%; Score 549; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.4e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 4
US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
```

```
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match      100.0%; Score 549; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.4e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 5
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020084528A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match      100.0%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 9.8e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60
Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 192
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 193 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238

RESULT 6
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
```


; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-9

Query Match 96.9%; Score 532; DB 10; Length 108;
Best Local Similarity 95.3%; Pred. No. 7.4e-30;
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
DB 61 FSGSGSGTSLTISRMEADAATYYCQORSTYPLTFGAGTKLEIK 106

RESULT 11

US-09-982-107-12
; Sequence 12; Application US/09982107
; Patent No. US20020159958A1

; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12

Query Match 94.4%; Score 518; DB 9; Length 105;
Best Local Similarity 93.3%; Pred. No. 6.3e-29;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
DB 1 DIWTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSLTISRMEADAATYYCQORSSYPFTFGSGTKLEI 105
DB 61 FSGSGSGTSLTISRMEADAATYYCHQRTSYPTFGGSGTKLEI 105

RESULT 12

US-09-807-724-2
; Sequence 2; Application US/09807721
; Patent No. US20020174453A1

; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY

; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,721
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-721-2

Query Match 94.4%; Score 518; DB 9; Length 669;
Best Local Similarity 92.5%; Pred. No. 2.5e-28;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
DB 457 DIVMTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 516
QY 61 FSGSGSGTSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
DB 517 FSGSGSGTSLTISRMEADAATYYCHQRTSYPTFGGSGTKLEIK 562

RESULT 13

US-09-144-886-88
; Sequence 88; Application US/09144886
; Patent No. US20020155114A1

; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/a clone
US-09-144-886-88

Query Match 92.7%; Score 509; DB 9; Length 107;
Best Local Similarity 97.0%; Pred. No. 2.5e-28;
Matches 97; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPCTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSLTISRMEADAATYYCQORSSYPFTFGSG 100
DB 61 FSGSGSGTSLTISRMEADAATYYCQORSSYPFTFGGG 100

RESULT 14

US-09-808-037-28
; Sequence 28; Application US/09808037
; Patent No. US20020052311A1

; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

```
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 119
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-808-037-28

Query Match          92.2%; Score 506; DB 10; Length 119;
Best Local Similarity 90.6%; Pred. No. 4.4e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTNLSGVPAR 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 14 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTNLSGVPAR 73
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 74 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGGGAKLEIK 119
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 15
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6

Query Match          92.2%; Score 506; DB 10; Length 239;
Best Local Similarity 90.6%; Pred. No. 7.4e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTNLSGVPAR 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 134 DIELTQSPAIMSASPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTNLSGVPAR 193
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGSGTKLEIK 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 194 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPPTFGGGAKLEIK 239
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:46-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-118/Region: complementarity-determining 3
F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 92.5%; Score 508; DB 2; Length 140;
Best Local Similarity 94.3%; Pred. No. 2.1e-34;
Matches 99; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSAPGKVTITCSASSVSYMHWFQOKPCTSPKLIWYTSNLSAGVPARF 61
Db 24 IVLTQSPAIMSAPGKVTITCSASSVSYMHWFQOKPCTSPKLIWYTSNLSAGVPVRF 83

QY 62 SGGSGTSTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 84 SGGSGTSTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 128

RESULT 3
A32513
Ig kappa chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: A32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: A32513
A:Molecule type: DNA
A:Residues: 1-130 <KOF>
A:Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 483; DB 2; Length 130;
Best Local Similarity 87.9%; Pred. No. 2.1e-33;
Matches 94; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSAPGKVTITCSASSV--SYMHWFQOKPCTSPKLIWYTSNLSAGVPA 59
Db 24 IVLTQSPAIMSAPGKVTITCSASSVSSSYLYWYQKPGSSPKLIWYTSNLSAGVPA 83

QY 60 RFGSGSGTSTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 84 RFGSGSGTSTSLTISRMEADAATYYCQYSGYPFTFGTKLEIK 130

RESULT 4
S05268
Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C:Accession: S05268; J10062; S03846
R:Levy, S.
submitted to the EMBL Data Library, February 1989
A:Reference number: S05267
A:Accession: S05268
A:Molecule type: mRNA
A:Residues: 1-132 <LEV>
A:Cross-references: EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261
R:Cartoll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A:Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explana
A:Reference number: J10061; MUID:89035985; PMID:3141553
A:Accession: J10062
A:Molecule type: mRNA
A:Residues: 1-120 <CAR>
A:Cross-references: EMBL:X14098

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:15-108/Domain: V region (V-kappa-1) <VRE>
F:30-103/Domain: immunoglobulin homology <IMM>
F:109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 88.0%; Score 483; DB 2; Length 132;
Best Local Similarity 85.8%; Pred. No. 2.1e-32;
Matches 91; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSAPGKVTITCSASSVSYMHWFQOKPCTSPKLIWYTSNLSAGVPAR 60
Db 15 EILTQSPAIMSAPGKVTITCSASSVSYMHWFQOKPCTSPKLIWYTSNLSAGVPAR 74

QY 61 FSGSGTSTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 75 FSGSGTSTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 120

RESULT 5
PC4405
Ig kappa chain V region (F3, anti-APP) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 21-Jan-2000
C:Accession: PC4405
R:Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A:Title: Generation of a phage display library of the immunoglobulin repertoire from
A:Reference number: PC4405
A:Accession: PC4405
A:Molecule type: mRNA
A:Residues: 1-107 <DEN>
A:Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 482; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.1e-32;
Matches 93; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSAPGKVTITCSASSVSYMHWFQOKPCTSPKLIWYTSNLSAGVPAR 60
Db 1 DIELTQSPAIMSAPGKVTITCSASSVSYMHWFQOKPCTSPKLIWYTSNLSAGVPAR 60

QY 61 FSGSGTSTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGTSTSLTISRMEADAATYYCQQRSDNPFTFGSGTKLEIK 106

RESULT 6
D38601
Ig kappa chain V region (6A7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: D38601
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: D38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <GOS>
A:Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 481; DB 2; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.3e-32;
Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Oy 9 AIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLWIYSTNLSAGVPARFSGSGT 68
|||||
Db 1 AIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLWISSTNLSAGVPARFSGSGT 60
|||||

Oy 69 SYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 61 SYSLTISRMEADAATYYCQHRSSYPYTFGGGTKLEIK 98
|||||

RESULT 7
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: A30562
R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: A30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 476; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 6.4e-32;
Matches 93; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Oy 2 IELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLWIYSTNLSAGVPARF 61
|
Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHWFQKPGTSPKRWIYDTSKLASGVPARF 61
|||||

Oy 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 62 SGSGSGTSYSLTISRMEADAATYYCQWSSNPYTFGGGTKLEIK 106
|||||

RESULT 8
G27887
Ig kappa chain V region (H18-S415) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: G27887
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a c
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: G27887
A:Molecule type: DNA
A:Residues: 1-106 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 474; DB 2; Length 106;
Best Local Similarity 84.8%; Pred. No. 9.2e-32;
Matches 89; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Oy 2 IELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLWIYSTNLSAGVPARF 61
|
Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHWFQKPGTSPKRWIYDTSKLASGVPTRF 61
|||||

Oy 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
||
Db 62 SGSGSGTSYSLTISRMEADAATYYCHORSYPLTFGGGTKLEIK 106
|||||
```

```
RESULT 9
PS0070
Ig kappa chain V region (38C13.V6.1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0070
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrang
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0070
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <LEF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 472; DB 2; Length 106;
Best Local Similarity 83.0%; Pred. No. 1.3e-31;
Matches 88; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Oy 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLWIYSTNLSAGVPAR 60
:|
Db 1 EIFLTQSPAILAASPGKVTITCSASSSVYMNWYQKPGSPKRWIYGTISNLSAGVPAR 60
|||||

Oy 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 61 FSGSGSGTSFSFTINSMEADVATYYCQQRSSYPFTFGAGTKLEIK 106
|||||

RESULT 10
B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30562
R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen
A:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: B30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 471; DB 2; Length 107;
Best Local Similarity 86.7%; Pred. No. 1.6e-31;
Matches 91; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 2 IELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLWIYSTNLSAGVPARF 61
|
Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHWFQKPGTSPKRWIYDTSKLASGVPTRF 61
|||||

Oy 62 SGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
|||||
Db 62 SGSGSGTSYSLTISRMEADAATYYCQWSSNPYTFGGGTKLEIK 106
|||||

RESULT 11
S26338
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26338
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
```

A:Accession: S26338
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-105 <STA>
A:Cross-references: EMBL:X59197; NID:g52328; PIDN:CA441907.1; PID:g1334069
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 470; DB 2; Length 105;
Best Local Similarity 88.3%; Pred. No. 1.9e-31;
Matches 92; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNSLASGVPARF 61
DB 2 IVLTQSPAIMSASPGKVTITCSASSSVSYMYWYQKPGSGSPRWIYRTNSLASGVPARF 61

QY 62 SGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 105
DB 62 SGSGSGTSLTISSEMEADAATYYCQYHSYPPTFGGKLEI 105

RESULT 12
S29591
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S29591
R:Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S29591
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <NAV>
A:Cross-references: EMBL:X59094; NID:g52227; PIDN:CA441820.1; PID:g52228
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match 84.7%; Score 465; DB 2; Length 103;
Best Local Similarity 88.3%; Pred. No. 4.8e-31;
Matches 91; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNSLASGVPARF 61
DB 1 IVLTQSPAIMSASPGKVTITCSASSSVSYMYWYQKSGTSPRWIYDTSKLASGVPARF 60

QY 62 SGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLE 104
DB 61 SGSGSGTSLTISSEMEADAATYYCQWSSNPLTFGAGTKLE 103

RESULT 13
PL0278
Ig kappa chain V region (anti-DNA, 3H9VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0278
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 285-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0278
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-91/Domain: immunoglobulin homology <IMM>
F:24-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-57/Region: complementarity-determining 2

F:58-89/Region: framework 3
F:90-98/Region: complementarity-determining 3
F:99-108/Region: framework 4

Query Match 84.7%; Score 465; DB 2; Length 108;
Best Local Similarity 86.7%; Pred. No. 5e-31;
Matches 91; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNSLASGVPARF 61
DB 4 LTQSPAIMSASPGKVTITCSADSSVSNFHWYQKPGTSPKLIWYSTNSLASGVPARF 63

QY 62 SGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 106
DB 64 SGSGSGTSLTISSEMEADAATYYCQWCGYPFTFGTKLEI 108

RESULT 14
JL0079
Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: JL0079; A49044; B49044
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-
A:Reference number: JL0076; MUID:89096973; PMID:3211160
A:Accession: JL0079
A:Molecule type: mRNA
A:Residues: 1-130 <KAA>
A:Cross-references: GB:M27792; NID:g197159
A:Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A:Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue
A:Note: the authors translated the codon TTT for residue 8 as Pro and TTC for residue
R:Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A:Title: Non-random features of the repertoire expressed by the members of one V kappa
A:Reference number: A49044; MUID:92289826; PMID:1601044
A:Accession: A49044
A:Molecule type: DNA
A:Residues: 1-25 <MTL>
A:Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250217
A:Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A:Accession: B49044
A:Molecule type: DNA
A:Residues: 114-116 <MTL2>
A:Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
A:Experimental source: BALB/c germ-line
A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 ad
A:Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
C:Genetics:
A:Gene: V(kappa)Ox1
A:Introns: 17/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (L)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide bonds: #status predicted

Query Match 84.5%; Score 464; DB 1; Length 130;
Best Local Similarity 86.7%; Pred. No. 7.1e-31;
Matches 91; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNSLASGVPARF 61
DB 24 IVLTQSPAIMSASPGKVTITCSASSSVSYMYWYQKSGTSPRWIYDTSKLASGVPARF 83

QY 62 SGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEI 106
DB 84 SGSGSGTSLTISSEMEADAATYYCQWSSNPLTFGAGTKLEI 128


```

RESULT 15
PS0071
Ig kappa chain V region (38C13.V8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0071
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0071
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match      84.3%; Score 463; DB 2; Length 106;
Best Local Similarity 86.7%; Pred. No. 7.le-31:
Matches 91; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy  2  IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYTSNLAGVPA RF 61
Db  2  IELTQSPAIMASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYTSNLAGVPA RF 61
Qy  62  SGSGSGTSYSLTISRMEAEADAATYCCQORSSYPFTFGSGTKLEIK 106
Db  62  SGSGSGTSYSLTISRMEAEADAATYCCQOWSSNPVTFGAPTKLEK 106

```

Search completed: December 23, 2002, 07:31:40
Job time : 21.9535 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17 ; Search time 10.4767 Seconds
(without alignments)
419.643 Million cell updates/sec

Title: US-09-865-198-23

Perfect score: 549

Sequence: 1 DIELTQSPALMSASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	457	83.2	107	1 KV6F_MOUSE	P04940 mus musculus
2	452	82.3	107	1 KV6I_MOUSE	P04943 mus musculus
3	452	82.3	107	1 KV6J_MOUSE	P04944 mus musculus
4	451	82.1	107	1 KV6H_MOUSE	P04942 mus musculus
5	450	82.0	107	1 KV6G_MOUSE	P04941 mus musculus
6	450	82.0	108	1 KV6K_MOUSE	P04945 mus musculus
7	428	78.0	107	1 KV6B_MOUSE	P01676 mus musculus
8	425	77.4	107	1 KV6A_MOUSE	P01675 mus musculus
9	424	77.2	107	1 KV6D_MOUSE	P01678 mus musculus
10	423	77.0	107	1 KV6C_MOUSE	P01677 mus musculus
11	408	74.3	107	1 KV6E_MOUSE	P01679 mus musculus
12	405	73.8	129	1 KV4A_MOUSE	P01680 mus musculus
13	373.5	68.0	111	1 KV3N_MOUSE	P01665 mus musculus
14	368.5	67.1	111	1 KV3O_MOUSE	P01667 mus musculus
15	366.5	66.8	111	1 KV3L_MOUSE	P01664 mus musculus
16	363.5	66.2	108	1 KV1V_HUMAN	P04430 homo sapien
17	363.5	66.2	111	1 KV3H_MOUSE	P01660 mus musculus
18	362.5	66.0	111	1 KV3J_MOUSE	P01662 mus musculus
19	362.5	66.0	111	1 KV3N_MOUSE	P01666 mus musculus
20	361.5	65.8	108	1 KV1Q_HUMAN	P01607 homo sapien
21	361.5	65.8	111	1 KV3Q_MOUSE	P01669 mus musculus
22	361.5	65.8	111	1 KV3S_MOUSE	P01671 mus musculus
23	360.5	65.7	131	1 KV3I_MOUSE	P01661 mus musculus
24	359.5	65.5	111	1 KV3R_MOUSE	P01670 mus musculus
25	358.5	65.3	111	1 KV3M_MOUSE	P01663 mus musculus
26	357.5	65.1	108	1 KV1B_HUMAN	P01594 homo sapien
27	357.5	65.1	129	1 KV1W_HUMAN	P04431 homo sapien
28	354.5	64.6	111	1 KV1T_MOUSE	P01672 mus musculus
29	354	64.5	110	1 KV3P_MOUSE	P01668 mus musculus
30	351.5	64.0	111	1 KV3U_MOUSE	P01673 mus musculus
31	350.5	63.8	108	1 KV5J_MOUSE	P01643 mus musculus
32	349.5	63.7	108	1 KV1H_HUMAN	P01600 homo sapien
33	349.5	63.7	111	1 KV3A_MOUSE	P01654 mus musculus

ALIGNMENTS

```
RESULT 1
KV6F_MOUSE
AC 04940; STANDARD; PRT; 107 AA.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazolone and its early diversification."
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC -----
CC EMBL; K00735; AAA38680.1; -.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC Immunoglobulin V region; Hybridoma.
CC DOMAIN 1 23
CC FRAMEWORK-1.
CC COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 24 33
CC FRAMEWORK-2.
CC COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 34 48
CC COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 49 55
CC FRAMEWORK-3.
CC COMPLEMENTARITY-DETERMINING-4.
CC DOMAIN 56 87
CC FRAMEWORK-4.
CC DISULFID 88 96
CC BY SIMILARITY.
CC FT DISULFID 23 87
CC NON_TER 107 107
CC SEQUENCE 107 AA; 11561 MW; 6F694284E6A8E6 CRC64;
Query Match 83.2%; Score 457; DB 1; Length 107;
Best Local Similarity 83.8%; Pred. No. 4.7e-39;
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy 2 IELTQSPALMSASPGKVTITCSASSSYHHWFQKPGTSPKLTWYTSNLSASGVPARF 61
Db 2 IVLTSQPAIMASPGKQVYTCSSASSSYHHWFQKPGTSPKLTWYTSNLSASGVPARF 61
Qy 62 SGSGSGTYSLSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
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 DR EMBL; K00739; AAA38684.1; -
 DR HSSP; P01679; 2FBJ
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 34 48 FRAMEWORK-2.
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 56 87 FRAMEWORK-3.
 FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 97 106 FRAMEWORK-4.
 FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;
 Query Match 82.1%; Score 451; DB 1; Length 107;
 Best Local Similarity 82.9%; Pred. No. 1.9e-38;
 Matches 87; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 QY 2 IELTQSPAIMSASPGKVTITCSASSSYVMHWFQKPGTSPKLIWYSTSLASGVPARF 61
 Db 2 IVLTQSPAIMSASPGKVTMTCSASSSYVMHWYQKSGTSPKRWIYDTSLKDSGVPARF 61
 QY 62 SGSGSGTSYSLTISRMEADAATYTCQORSSYPPTFGSGTKLEIK 106
 Db 62 SGSGSATSYSLTISMQAEDAATYTCQOWSSNPLTFGAGTKLEK 106
 RESULT 5
 KV6G_MOUSE
 ID KV6G_MOUSE STANDARD; PRT; 107 AA.
 AC P04941;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-VI region NQ2-48.2.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification."
 RL Nature 304:320-324(1983).
 CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
 CC
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 DR EMBL; K00737; AAA38682.1; -
 DR HSSP; P01679; 2FBJ
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.

Immunoglobulin V region; Hybridoma.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 34 48 FRAMEWORK-2.
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 56 87 FRAMEWORK-3.
 FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 97 106 FRAMEWORK-4.
 FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;
 Query Match 82.0%; Score 450; DB 1; Length 107;
 Best Local Similarity 82.9%; Pred. No. 2.4e-38;
 Matches 87; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 QY 2 IELTQSPAIMSASPGKVTITCSASSSYVMHWFQKPGTSPKLIWYSTSLASGVPARF 61
 Db 2 ILLTQSPAIMSASPGKVTMTCSASSSYVMHWYQKSGTSPKRWIYDTSLASGVPARF 61
 QY 62 SGSGSGTSYSLTISRMEADAATYTCQORSSYPPTFGSGTKLEIK 106
 Db 62 SGSGSATSYSLTISMQAEDAATYTCQOWSSNPLTFGAGTKLXLK 106
 RESULT 6
 KV6K_MOUSE
 ID KV6K_MOUSE STANDARD; PRT; 108 AA.
 AC P04945;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-VI region NQ2-6.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification."
 RL Nature 304:320-324(1983).
 CC
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 DR EMBL; K00746; AAA38691.1; -
 DR HSSP; P01679; 2FBJ
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 34 48 FRAMEWORK-2.
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 56 87 FRAMEWORK-3.
 FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 99 108 FRAMEWORK-4.
 FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
 Query Match 82.0%; Score 450; DB 1; Length 108;
 Best Local Similarity 82.2%; Pred. No. 2.4e-38;


```
RT "Rearrangement of genetic information may produce immunoglobulin
RL diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 67.18; Score 368.5; DB 1; Length 111;
Best Local Similarity 64.9%; Pred. No. 3.4e-30;
Matches 72; Conservative 14; Mismatches 20; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSV----SYMHWFQOKPCTSPKLIYTSNLS 55
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGSIMNMYQOKPGQPKLIYTSNLS 60

Qy 56 GVPARFSGSGSTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
Db 61 GIPARFSGSGSTDFTLNIHPVEEDAATYYCQSNEDPYTFGGTKLEIK 111

RESULT 15
KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1995 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT-TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 66.8%; Score 366.5; DB 1; Length 111;
```

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Best Local Similarity 64.0%; Pred. No. 5.3e-30;
Matches 71; Conservative 14; Mismatches 21; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSV----SYMHWFQOKPCTSPKLIYTSNLS 55
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGSIMNMYQOKPGQPKLIYTSNLS 60

Qy 56 GVPARFSGSGSTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
Db 61 GIPARFSGSGSTDFTLNIHPVEEDAATYYCQSNEDPYTFGGTKLEIK 111
```

Search completed: December 23, 2002, 07:26:14
Job time : 11.4767 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:27 ; Search time 43.9612 Seconds
(without alignments)
496.824 Million cell updates/sec

Title: US-09-865-198-23

Perfect score: 549

Sequence: 1 DIELTOSPAIMSASPGKVT.....CQORSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493	89.8	134	11 Q8VDD0	Q8vdd0 mus musculu
2	470	85.6	106	5 Q9U410	Q9u410 schistosoma
3	434	79.1	97	11 Q9JL76	Q9jl76 mus musculu
4	433	78.9	235	11 Q9LW12	Q9lw12 mus musculu
5	403.5	73.5	101	11 Q9JL78	Q9jl78 mus musculu
6	371.5	67.7	234	11 Q8R062	Q8r062 mus musculu
7	365.5	66.6	111	11 Q920E9	Q920e9 mus musculu
8	362.5	66.0	214	11 Q9R1A5	Q9rla5 mus musculu
9	360.5	65.7	108	4 Q9UL77	Q9ul77 homo sapien
10	356	64.8	107	4 Q96SA9	Q96sa9 homo sapien
11	356	64.8	109	4 Q9UL78	Q9ul78 homo sapien
12	354.5	64.6	108	4 Q9UL70	Q9ul70 homo sapien
13	352.5	64.2	108	4 Q9UL79	Q9ul79 homo sapien
14	348	63.4	107	4 Q9UL81	Q9ul81 homo sapien
15	347.5	63.3	234	11 Q9LWF8	Q9lwf8 mus musculu
16	347.5	63.3	234	11 Q8VCP0	Q8vcp0 mus musculu

17	345.5	62.9	233	11 Q91WS9	Q91ws9 mus musculu
18	342.5	62.4	107	11 Q9JL84	Q9jl84 mus musculu
19	342.5	62.4	298	11 Q9QVFO	Q9qvfo mus musculu
20	341.5	62.2	108	4 Q9UL83	Q9ul83 homo sapien
21	338.5	61.7	109	11 Q920E6	Q920e6 mus musculu
22	337	61.4	109	4 Q9UL86	Q9ul86 homo sapien
23	332.5	60.6	108	11 Q8VIJ0	Q8vij0 mus musculu
24	332	60.5	109	4 Q9UL85	Q9ul85 homo sapien
25	322	58.7	238	11 Q9NM37	Q9nm37 mus musculu
26	321.5	58.6	127	11 Q925S9	Q925s9 mus musculu
27	315.5	57.5	116	4 Q96PF6	Q96pf6 homo sapien
28	314	57.2	238	11 Q8VC16	Q8vc16 mus musculu
29	308.5	56.2	103	11 Q9JL80	Q9jl80 mus musculu
30	304	55.4	239	11 Q8VC55	Q8vc55 mus musculu
31	302	55.0	239	4 Q8TCD0	Q8tcd0 homo sapien
32	300.5	54.7	107	11 Q9ERZ9	Q9erz9 mus musculu
33	297	54.1	104	11 Q9JL82	Q9jl82 mus musculu
34	292.5	53.3	99	11 Q9JL74	Q9jl74 mus musculu
35	290.5	52.9	114	4 Q9UL80	Q9ul80 homo sapien
36	286	52.1	241	11 Q921A6	Q921a6 mus musculu
37	281	51.2	237	4 Q8WTU6	Q8wtu6 homo sapien
38	277.5	50.5	234	11 Q8R028	Q8r028 mus musculu
39	276	50.3	237	4 Q8WUK4	Q8wuk4 homo sapien
40	260.5	47.4	109	6 Q9N0W5	Q9n0w5 oryctolagus
41	259	47.2	233	4 Q8TBC9	Q8tbc9 homo sapien
42	247.5	45.1	236	4 Q96E61	Q96e61 homo sapien
43	244	44.4	107	4 Q9NSD6	Q9nsd6 homo sapien
44	244	44.4	110	4 Q8TE63	Q8te63 homo sapien
45	243	44.3	108	4 Q96SB0	Q96sb0 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8VDD0	PRELIMINARY;	PRT;	134 AA.
AC	Q8VDD0;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Anti-MOG z12 variable light chain (Fragment).			
GN	ANTI-MOG KAPPA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RA	Sembi P.;			
RT	"Targeting T cells to the CNS."			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBDJ databases.			
DR	EMBL; AJ416331; CAC94866.1; -			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00409; Ig; 1.			
DR	SMART; SM00406; Ig; 1.			
FT	NON_TER 134 134			
SQ	SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;			

Query Match 89.8%; Score 493; DB 11; Length 134;
Best Local Similarity 89.5%; Pred.No. 2.4e-44;
Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 IELTOSPAIMSASPGKVTITCSASSSVSYMHWFQOKFGTSPKLIWYSTNLSAGVPARF 61

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Db 24 IVLTQSPALMSASPGKVTITCSASSSYMHYQQRPGTSPKRWIYDTSKLASGVPARF 83
QY 62 SGSGSGTYSYLTIISRMEDAAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 84 SGSGSGTYSYLTIISRMEDAAATYYCQQRSSYPFTFGSGTKLEIK 128

RESULT 2
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment)
OS Schistosoma japonicum (Blood fluke)
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Acc:207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 106
FT NON_TER 1 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 85.6%; Score 470; DB 5; Length 106;
Best Local Similarity 87.4%; Pred. No. 4.8e-42;
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPALMSASPGKVTITCSASSSYMHYQQRPGTSPKLIYSTNLSAGVPARFSG 63
Db 4 LTQSPALMSASPGKVTITCSASSSYMHYQQRPGTSPKLIYSTNLSAGVPARFSG 63

QY 64 SGSGTYSYLTIISRMEDAAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 64 SGSGTYSYLTIISRMEDAAATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 3
Q9JL76
ID Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Walkiel S., Liao L., Cunningham M.W., Diamond B.;
RX MEDLINE=20448942; PubMed=10992488;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
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DR EMBL; AF206030; AAF69328.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 97
FT NON_TER 1 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFELF49DAIC CRC64;

Query Match 79.1%; Score 434.5; DB 11; Length 97;
Best Local Similarity 86.6%; Pred. No. 2.3e-38;
Matches 84; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 11 MSASPGKVTITCSASSSYMHYQQRPGTSPKLIYSTNLSAGVPARFSGSGTYSY 70
Db 1 LSASPGKVTITCRASSSYMHYQQRPGTSPKLIYSTNLSAGVPARFSGSGTYSY 60

QY 71 SLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 SLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 97

RESULT 4
Q9LW12
ID Q9LW12 PRELIMINARY; PRT; 235 AA.
AC Q9LW12;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=BREAST TUMOR;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 78.9%; Score 433; DB 11; Length 235;
Best Local Similarity 81.0%; Pred. No. 9.7e-38;
Matches 85; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPALMSASPGKVTITCSASSSYMHYQQRPGTSPKLIYSTNLSAGVPARF 61
Db 24 IVLTQSPALMSASPGKVTITCSASSSYMHYQQRPGTSPKLIYSTNLSAGVPARF 83

QY 62 SGSGSGTYSYLTIISRMEDAAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 84 SGSGSGTYSYLTIISRMEDAAATYYCQQRSSYPFTFGSGTKLEIK 128

RESULT 5
Q9JL78
ID Q9JL78 PRELIMINARY; PRT; 101 AA.
AC Q9JL78;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206028; AAF69326.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 101
FT SEQUENCE 101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;

Query Match 73.5%; Score 403.5; DB 11; Length 101;
Best Local Similarity 80.8%; Pred. No. 4.5e-35;
Matches 80; Conservative 6; Mismatches 10; Indels 3; Gaps 2;

Qy 11 MSASPGKVTITCSASSSV--YMHWFQOKPGTSPKLIWYSTNLSAGVPAFSGSGGT 68
Db 3 MAASPGKVTITCSASSSVISNLYHWYQKPGFSPKLIYRTSNLSAGVPTFSGSGGT 62

Qy 69 SYSLTISRMEADAATYYCQQRSSYP-FTFGSGTKLEIK 106
Db 63 SYSLTIGTMEADVATYYCQGSISIPRTFTGGTKLEIK 101

RESULT 6
Q9R062
ID Q9R062 PRELIMINARY; PRT; 234 AA.
AC Q9R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 67.7%; Score 371.5; DB 11; Length 234;
Best Local Similarity 67.3%; Pred. No. 2.9e-31;
Matches 72; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSSV--YMHWFQOKPGTSPKLIWYSTNLSAGVPA 59
Db 21 DIQMTQTSSLSASLGDRVTITCSASQGISNLYNWKQKPGDGTVKLLIYRTSNLSHSGVPS 80

Qy 60 RFGSGSGTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 81 RFGSGSGTHYSLTISNLEPDATYYCQYSQFPFTFGSGTKLEIK 127

RESULT 7
Q920E9
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
```

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DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 111
FT SEQUENCE 111 AA; 12046 MW; 1E46988AA685826 CRC64;

Query Match 66.6%; Score 365.5; DB 11; Length 111;
Best Local Similarity 64.9%; Pred. No. 5.1e-31;
Matches 72; Conservative 10; Mismatches 24; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSV----SYMHWFQOKPGTSPKLIWYSTNLSAS 55
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWFQOKPGQPKLLIYLASNLES 60

Qy 56 GVPARFSGSGTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 GVPARFSGSGGTFTLNIHPVEEDAATYYCQHSRELPTFTGGTKLEIK 111

RESULT 8
Q9RIA5
ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Mistra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
FT SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 66.0%; Score 362.5; DB 11; Length 214;
Best Local Similarity 66.4%; Pred. No. 2.3e-30;
Matches 71; Conservative 9; Mismatches 26; Indels 1; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKVTITCSASSSV--SYMHWFQOKPGTSPKLIWYSTNLSAGVPA 59
Db 1 DIQLTQSPSSMYASLGERVTITCKAQDINSYLSWFWQKPGKSPKLIYRANRLVDGVPS 60

Qy 60 RFGSGSGTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
Db 61 RFGSGSGTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
```

Db 61 RFGSGSGQDYSLTATISSLEVEDMGIYCLQYDEPFTFGSGTKLEIK 107

RESULT 9

Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77; (Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -;
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 55.7%; Score 360.5; DB 4; Length 108;

Best Local Similarity 63.6%; Pred. No. 1.7e-30;
Matches 68; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIETQSPALMSASPGKVTITCSASSV--SYMHWFQOKPGTSPKLIWYSTSLASGVPA 59
||:||||: ||| ||:||||| || ||:||||| ||:||||| ||:||||| ||:|||||
Db 1 DIQWQSPSSLSASVGRVITTCRASQSISSYLNWYQOKPGKAPNLLIYAASSLQSGVPS 60
||:||||: ||| ||:||||| || ||:||||| ||:||||| ||:||||| ||:|||||
QY 60 RFGSGSGTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
||||||| :||||: || ||||| || ||||| || ||||| || ||||| || |||||
Db 61 RFGSGSGTDTLTITISLQPEDFATYYCQSQSYSTFWFGSGTKVEIK 107

RESULT 10

Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9; (Created)
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; Y06396; AAB68785.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
SQ SEQUENCE 107 107

SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 64.8%; Score 356; DB 4; Length 107;
Best Local Similarity 64.5%; Pred. No. 4.9e-30;
Matches 69; Conservative 19; Mismatches 17; Indels 2; Gaps 2;

QY 1 DIETQSPALMSASPGKVTITCSASSV--SYMHWFQOKPGTSPKLIWYSTSLASGVPA 59
||:||||: ||| ||:||||| || ||:||||| ||:||||| ||:||||| ||:|||||
Db 1 DIQWQSPSSLSASVGRVITTCRASQSISSYLNWYQOKPGKAPNLLIYAASSLQSGVPS 60
||:||||: ||| ||:||||| || ||:||||| ||:||||| ||:||||| ||:|||||
QY 60 RFGSGSGTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
||||||| :||||: || ||||| || ||||| || ||||| || ||||| || |||||
Db 61 RFGSGSGTDTLTITISLQPEDFATYYCQSQSYSTFWFGSGTKVEIK 106

RESULT 11

Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78; (Created)
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -;
DR HSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52ECTEE197 CRC64;

Query Match 64.8%; Score 356; DB 4; Length 109;
Best Local Similarity 62.0%; Pred. No. 5e-30;
Matches 67; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

QY 1 DIETQSPALMSASPGKVTITCSASSV--SYMHWFQOKPGTSPKLIWYSTSLASGVPA 58
||:||||: ||| ||:||||| || ||:||||| ||:||||| ||:||||| ||:|||||
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQOKPGAPRLLIYGASSRATGIP 60
||:||||: ||| ||:||||| || ||:||||| ||:||||| ||:||||| ||:|||||
QY 59 ARFSGSGSTYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
||||||| :||||: || ||||| || ||||| || ||||| || ||||| || |||||
Db 61 DRFSGSGSGTDTLTITISRLPEPCAVYCCQYQSSPLTFGGGTVKVEIK 108

RESULT 12

Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70; (Created)
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 64.6%; Score 354.5; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 7.1e-30;
Matches 68; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

Qy 1 DIETQSPAINASGPEKVTITCSASSVS-YMHWFQOKPGTSPKLIWYSTSNLASGVPA 59
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNLYAWYQOKPGKPKSLIYAASSTLQSGVPS 60

Qy 60 RFSGGSGTSTSLTISRMEADAATYYCQORSSYPFFTSGSTKLEIK 106
Db 61 RFSGGSGTDTFTLTISLQSEDVATYYCQKYNAPRIFGPGTKLEIK 107

RESULT 13
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 64.2%; Score 352.5; DB 4; Length 108;
Best Local Similarity 61.7%; Pred. No. 1.2e-29;
Matches 66; Conservative 21; Mismatches 19; Indels 1; Gaps 1;

Qy 1 DIETQSPAINASGPEKVTITCSASSV-SYMHWFQOKPGTSPKLIWYSTSNLASGVPA 59
Db 1 DIVMTQSPSLLSASGDRVTITCRMSQGISNLYAWYQOKPGKAPPELLIYAASSTLQSGVPS 60

Qy 60 RFSGGSGTSTSLTISRMEADAATYYCQORSSYPFFTSGSTKLEIK 106
Db 61 RFSGGSGTDTFTLTISLQSEDVATYYCQYSPFFTSGSTKLEIK 107
```

```
RESULT 14
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 63.4%; Score 348; DB 4; Length 107;
Best Local Similarity 62.6%; Pred. No. 3.4e-29;
Matches 67; Conservative 21; Mismatches 17; Indels 2; Gaps 2;

Qy 1 DIETQSPAINASGPEKVTITCSASSVS-YMHWFQOKPGTSPKLIWYSTSNLASGVPA 59
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNLYAWYQOKPGKAPNLLIYAASSTLQSGVPS 60

Qy 60 RFSGGSGTSTSLTISRMEADAATYYCQORSSYPFFTSGSTKLEIK 106
Db 61 RFSGGSGTDTFTLTISLQAEAFATYYCQSYS-ALTEGPGTKVDIR 106

RESULT 15
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR Hypothetical protein.
KW SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 63.3%; Score 347.5; DB 11; Length 234;
Best Local Similarity 62.6%; Pred. No. 9.8e-29;
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Matches 67; Conservative 19; Mismatches 20; Indels 1; Gaps 1;
Qy 1 DIELTQSPAINSPGKVTITCSASSVS-YMHWFQOKPCTSPKLMWYTSNLAGVPA 59
Db 21 DIOMTOTTSSLASLGRVTISCRASODISNYLNWYQOKPDGTVKLLIYYTSRLYLGVP 80
Qy 60 RFSGSGSTSYSLTISRMEADAATYCCQORSYPPFTFGSGTKLEIK 106
Db 81 RFSGSGSTDYSLTISNLEQEDATYCCQGNTPPFTFGSGTKLEV 127

Search completed: December 23, 2002, 07:29:59
Job time : 43.9612 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 : Search time 4.8314 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-6

Perfect score: 48

Sequence: 1 QORSSYPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	21	AA97234
2	48	100.0	9	22	AAE13142
3	48	100.0	9	22	AAE13142
4	48	100.0	9	22	AAE13142
5	48	100.0	9	22	AAE13142
6	48	100.0	106	22	AAE13144
7	48	100.0	106	22	AAE13148
8	48	100.0	107	22	AAE13148
9	48	100.0	108	21	AA97236
10	48	100.0	108	22	AAE13140

11	48	100.0	108	23	AAU74413	Antigen-binding pr
12	48	100.0	125	22	AAE13146	Chimeric p1c11 lig
13	48	100.0	125	22	AAE13146	VEGF antagonist an
14	48	100.0	238	23	AAU74420	Antigen-binding pr
15	48	100.0	240	23	AAU74419	Antigen-binding pr
16	48	100.0	330	22	AAU70842	SNV-env leader/hum
17	45	93.8	9	19	AAU73171	CDR3 of light cha
18	45	93.8	9	20	AAU73171	Peptide fragment f
19	45	93.8	9	22	AAE13145	Mouse ganglioside
20	45	93.8	107	22	AAE13159	Mouse ganglioside
21	45	93.8	107	22	AAE13167	Ganglioside GM2 an
22	45	93.8	129	15	AAU53329	KM-796 and KM-750
23	45	93.8	129	20	AAU28385	Anti-GM2 light cha
24	45	93.8	129	20	AAU28357	Antibody chain use
25	45	93.8	130	19	AAU73179	Fragment of gangli
26	45	93.8	130	19	AAU73180	Fragment of gangli
27	45	93.8	130	19	AAU73181	Fragment of gangli
28	45	93.8	130	19	AAU73182	Fragment of gangli
29	45	93.8	130	19	AAU73183	Fragment of gangli
30	45	93.8	130	19	AAU73184	Fragment of gangli
31	45	93.8	130	19	AAU73185	Fragment of gangli
32	45	93.8	130	19	AAU73173	Light chain of gan
33	45	93.8	130	19	AAU73174	Light chain of gan
34	45	93.8	130	19	AAU73176	Light chain of gan
35	45	93.8	130	20	AAU28375	Human chimeric ant
36	45	93.8	130	20	AAU28376	Human chimeric ant
37	45	93.8	130	20	AAU28377	Human chimeric ant
38	45	93.8	130	20	AAU28378	Human chimeric ant
39	45	93.8	130	20	AAU28379	Human chimeric ant
40	45	93.8	130	20	AAU28380	Human chimeric ant
41	45	93.8	130	20	AAU28381	Human chimeric ant
42	45	93.8	130	20	AAU28382	Human chimeric ant
43	45	93.8	130	20	AAU28383	Human chimeric ant
44	45	93.8	133	15	AAU53345	REI human Ab L cha
45	45	93.8	133	20	AAU28394	Anti-GM2 light cha

ALIGNMENTS

RESULT 1

AA97234

ID AA97234 standard; Protein; 9 AA.

XX AC AA97234;

XX DT 19-DEC-2000 (first entry)

XX Complementary determining region (CDRL3) of anti-SI(KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR;

KW VEGF; vascular endothelial growth factor; KDR;

KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diadobody; triadobody;

KW glioblastoma multiforme; hemangioblastoma; AIDS;

KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;

KW acquired immune deficiency syndrome; AIDS; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200044777-A1.

XX PD 03-AUG-2000.

XX PF 28-JAN-2000; 2000WO-US02180.

XX PR 29-JAN-1999; 99US-0117726.

XX PR 29-JAN-1999; 99US-0240736.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z, Witte L;

```

XX DR WPI: 2000-505966/45.
XX DR N-PSDB; AAA53766.
XX PT Novel immunoglobulin molecules binding kinase insert domain-containing
XX PT receptor with the same affinity as vascular endothelial growth factor,
XX PT used to reduce tumour growth
XX PS Claim 3; Page 50; 55pp; English.
XX CC New immunoglobulin molecules are described that bind kinase insert
XX CC domain-containing receptor (KDR) with a comparable affinity to human
XX CC vascular endothelial growth factor (VEGF). The antibodies neutralise
XX CC KDR activation. The immunoglobulin may be a multivalent single
XX CC chain antibody, a monovalent single chain antibody, a diabody, a
XX CC triabody, a humanised antibody or a chimerised antibody.
XX CC The immunoglobulin molecules bind specifically to an
XX CC extracellular domain of the KDR receptor with the same affinity as
XX CC VEGF. Overexpression of VEGF has been implicated in a number of
XX CC human tumour cell lines including glioblastoma multiforme,
XX CC hemangioblastoma, central nervous system neoplasms and AIDS
XX CC associated Kaposi's sarcoma. The antibodies therefore have
XX CC applications in treating these conditions. This sequence encodes a
XX CC preferred heavy chain complementary determining region of the
XX CC immunoglobulins of the invention.
XX SQ Sequence 9 AA;
      Query Match 100.0%; Score 48; DB 21; Length 9;
      Best Local Similarity 100.0%; Pred. No. 7.8e+05;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
Db 1 QQRSSYPFT 9
      |||||
RESULT 2
AAE13142
ID AAE13142; standard; peptide; 9 AA.
AC AAE13142;
XX 28-JAN-2002 (first entry)
XX Humanised antibody murine light chain hypervariable region (VL) CDR3.
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytotaxtic; light chain hypervariable region; VL; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.
XX OS Mus sp.
XX WO200174296-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10504.
XX 31-MAR-2000; 2000US-0540770.
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (CORR ) CORNELL RES FOUND INC.
XX Witte I, Rafil S;
XX WPI: 2001-662942/76.
XX DR N-PSDB; AAD21668.
XX PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
XX PT tumors such as leukemias or multiple myeloma comprises treatment with
XX PT an antagonist of a vascular endothelial growth factor receptor -

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XX Claim 8; Page 15; 68pp; English.
XX The invention relates to a method for inhibiting the growth of non-solid
XX tumour cells that are stimulated by a ligand of vascular endothelial
XX growth factor receptor (VEGFR) in mammals particularly humans. The method
XX involves treating the mammals with humanised VEGFR monoclonal antibodies
XX (antagonists). Humanised monoclonal antibody comprises humanised mouse
XX variable region joined to human constant region, where the humanised
XX mouse variable region contains mouse complementarity determining region
XX (CDR) grafted into human variable region. The method is useful for
XX treating leukaemias such as acute or chronic myelocytic leukaemia, acute
XX or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
XX multiple myelomas and lymphoid cells, particularly those related to
XX non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
XX antibody murine light chain hypervariable region (VL) CDR-3 used in the
XX exemplification of the invention.
XX SQ Sequence 9 AA;
      Query Match 100.0%; Score 48; DB 22; Length 9;
      Best Local Similarity 100.0%; Pred. No. 7.8e+05;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
Db 1 QQRSSYPFT 9
      |||||
RESULT 3
AAB82708
ID AAB82708; standard; Peptide; 9 AA.
XX AAB82708;
XX 15-OCT-2001 (first entry)
XX VEGF antagonist antibody IMC-1C11 VL CDR-3.
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
KW complementarity determining region.
XX OS Chimeric - Mus sp.
XX OS Chimeric - Homo sapiens.
XX WO200154723-A1.
XX 02-AUG-2001.
XX 29-JAN-2001; 2001WO-US02839.
XX 28-JAN-2000; 2000US-0178791.
XX 31-MAR-2000; 2000US-0539692.
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
XX (IMCL-) IMCLONE SYSTEMS INC.
XX Kerbel R;
XX WPI: 2001-514531/56.
XX Treating or controlling an angiogenic dependent condition (e.g. a
XX PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
XX PT administering a combination of an antiangiogenic molecule and a
XX PT chemotherapeutic agent -
XX Disclosure; Page 37; 42pp; English.
XX

```

CC The present sequence is that of complementarity determining region
 CC 3 of the light chain variable region (see also AAB82702) of
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,
 CC or a fragment of it, can be used as an anti-angiogenic molecule,
 CC together with a chemotherapeutic acid, for the treatment of an
 CC angiogenic dependent condition in a mammal, especially a human.
 CC The invention relates generally to a method of treating or
 CC controlling an angiogenic dependent condition by administering an
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
 CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The anti-angiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
 | | | | | | | |
 Db 1 QORSSYPFT 9

RESULT 4
 AAG63993
 ID AAG63993 standard; peptide; 9 AA.

XX AC AAG63993;
 XX 26-NOV-2001 (first entry)
 XX Complementarity determining region of light chain of antibody 2C4.
 DE Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
 KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
 KW leukemia; eosinophil.
 XX Mus sp.
 OS
 XX WO200166126-A1.
 PN
 XX 13-SEP-2001.
 PD
 XX 05-MAR-2001; 2001WO-US07193.
 PF
 XX 07-MAR-2000; 2000US-0187595.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
 PI Schleimer R;
 PI
 XX WPI: 2001-570749/64.
 DR
 XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for
 PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
 PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal
 XX Claim 10; Page 34; 35pp; English.
 PS AAG63991-93 represent the complementarity determining regions (CDRs)
 XX of the light chain variable region of murine monoclonal antibody 2C4.
 CC

CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The
 CC antibody is useful for treating or preventing allergic rhinitis,
 CC allergies, asthma, anemia, eczema or diseases such as lymphoma,
 CC leukemia or systemic mastocytosis in a mammal. It is also useful for
 CC detecting the presence of a cell, especially eosinophil in a sample,
 CC by detecting binding of the antibody to SAF-2. The antibody can be
 CC coupled to toxins, antiproliferative drugs or radionuclides to
 CC kill cells in areas of excessive SAF-2 expression.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 48; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
 | | | | | | | |
 Db 1 QORSSYPFT 9

RESULT 5
 AAU74411
 ID AAU74411 standard; peptide; 9 AA.
 XX AC AAU74411;
 XX 26-MAR-2002 (first entry)
 DT
 XX Light chain complementarity determining region L3 (CDRL3).
 DE Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
 KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
 KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
 KW antibody light chain variable domain.
 XX Mus sp.
 OS
 XX WO200190192-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 24-MAY-2001; 2001WO-US16924.
 PF
 XX 24-MAY-2000; 2000US-206749P.
 PR
 XX (IMCL-) IMCLONE SYSTEMS INC.
 PA
 XX Zhu Z;
 PI
 XX WPI: 2002-106189/14.
 DR N-PSDB; AAS20282.
 DR
 XX New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides
 XX Claim 55; Page 57; 64pp; English.
 PS
 XX The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (Cl domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC

CC and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This peptide sequence represents the light chain variable domain complementary determining region L3 (CDRL3) incorporated into an antigen-binding protein described in the method of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | |
DB 1 QORSSYPFT 9

RESULT 6

ID AAE13144 standard; Protein; 106 AA.

XX AAE13144

DT 28-JAN-2002 (first entry)

DE Humanised antibody light chain fragment.

KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
human; chimeric.

OS Chimeric - Homo sapiens.
XX Chimeric - Mus sp.

XX WO200174296-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.
(CORR) CORNELL RES FOUND INC.

XX Witte L, Rafil S;

XX WPI: 2001-662942/76.
XX N-PSDB: AAD21670.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor.

XX Claim 8; Page 16; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody light chain fragment used in the exemplification of the invention.

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 48; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.073; 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9
| | | | | | | | | |
DB 88 QORSSYPFT 96

RESULT 7

ID AAU74418 standard; peptide; 106 AA.

XX AAU74418;

XX 26-MAR-2002 (first entry)

DE Antigen-binding protein light chain variable domain (VH) #2.

KW Antigen-binding protein; antibody light chain variable domain;
cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
cell proliferation inhibitor.

XX Mus sp.

XX WO200190192-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US16924.

XX 24-MAY-2000; 2000US-206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z;

XX WPI: 2002-106189/14.
XX N-PSDB: AAU20289.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides

XX Claim 61; Page 61; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.

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XX SQ Sequence 106 AA;
Query Match 100.0%; Score 48; DB 23; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 8
AAG63987
ID AAG63987 standard; Protein; 107 AA.
XX AC AAG63987;
XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of light chain variable region of antibody 2C4.
XX KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
XX KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
XX KW leukemia; eosinophil.
XX OS Mus sp.
XX XX WO200166126-A1.
XX PN 13-SEP-2001.
XX PD 05-MAR-2001; 2001WO-US07193.
XX PR 07-MAR-2000; 2000US-0187595.
XX XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX XX Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
XX PI Schleimer R;
XX DR WPI; 2001-570749/64.
XX DR N-PSDB; AAH78184.
XX XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for
XX PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
XX PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal -
XX PS Claim 11; Fig 2; 35pp; English.
XX CC The present sequence represents the light chain variable region of murine
XX CC monoclonal antibody 2C4. This antibody binds to human sialoadhesin
XX CC factor-2 (SAF-2). The antibody is useful for treating or preventing
XX CC allergic rhinitis, allergies, asthma, anemia, eczema or diseases such
XX CC as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also
XX CC useful for detecting the presence of a cell, especially eosinophil in
XX CC a sample, by detecting binding of the antibody to SAF-2. The antibody
XX CC can be coupled to toxins, antiproliferative drugs or radionuclides to
XX CC kill cells in areas of excessive SAF-2 expression.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 48; DB 22; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 9
AA97236
ID AA97236 standard; Protein; 108 AA.
XX AC AA97236;
XX DT 19-DEC-2000 (first entry)
XX DE Variable light chain fragment of anti-SI(KDR) antibody.
XX KW Immunoglobulin; antibody; complementary determining region; CDR;
XX KW VEGF; vascular endothelial growth factor; KDR;
XX KW kinase insert domain containing receptor; multivalent; monovalent;
XX KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
XX KW glioblastoma multiforme; hemangioblastoma; AIDS;
XX KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
XX KW acquired immune deficiency syndrome; AIDS; human.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX WO200044777-A1.
XX PN 03-AUG-2000.
XX PD 28-JAN-2000; 2000WO-US02180.
XX PR 29-JAN-1999; 99US-0117726.
XX PR 29-JAN-1999; 99US-0240736.
XX XX (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z, Witte L;
XX DR WPI; 2000-505966/45.
XX DR N-PSDB; AAA53768.
XX XX Novel immunoglobulin molecules binding kinase insert domain-containing
XX PT receptor with the same affinity as vascular endothelial growth factor,
XX PT used to reduce tumour growth
XX PS Claim 4; Page 51; 55pp; English.
XX CC New immunoglobulin molecules are described that bind kinase insert
XX CC domain-containing receptor (KDR) with a comparable affinity to human
XX CC vascular endothelial growth factor (VEGF). The antibodies neutralise
XX CC KDR activation. The immunoglobulin may be a multivalent single
XX CC chain antibody, a monovalent single chain antibody, a diabody, a
XX CC triabody, a humanised antibody or a chimerised antibody.
XX CC The immunoglobulin molecules bind specifically to an
XX CC extracellular domain of the KDR receptor with the same affinity as
XX CC VEGF. Overexpression of VEGF has been implicated in a number of
XX CC human tumour cell lines including glioblastoma multiforme,
XX CC hemangioblastoma, central nervous system neoplasms and AIDS
XX CC associated Kaposi's sarcoma. The antibodies therefore have
XX CC applications in treating these conditions. This sequence encodes a
XX CC preferred heavy chain complementary determining region of the
XX CC immunoglobulins of the invention.
XX SQ Sequence 108 AA;
Query Match 100.0%; Score 48; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
Db 88 QORSSYPFT 96

RESULT 10
AAB82710
ID AAB82710 standard; Protein; 108 AA.
```


Query Match 100.0%; Score 48; DB 23; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
 | | | | | | | | | |
Db 88 QORSSYPFT 96

RESULT 12
ID AAE13146
XX AAE13146 standard; Protein; 125 AA.
AC AAE13146;
XX
DT 28-JAN-2002 (first entry)
XX
DE Chimeric pIC11 light chain fragment.
XX
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytosatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human; pIC11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader_peptide
FT Protein 20..125
FT /note= "Mature chimeric pIC11 light chain fragment"
FT Region 43..52
FT /label= CDR_L1
FT Region 68..74
FT /label= CDR_L2
FT Region 107..115
FT /label= CDR_L3
XX
PN WO200174296-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10504.
XX
PR 31-MAR-2000; 2000US-0540770.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Witte L, Rafii S;
XX
DR WPI; 2001-662942/76.
DR N-PSDB; AAD21683.
XX
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Example 3; Fig 11; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to

CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC pIC11 light chain fragment which is used for the construction of chimeric
CC pIC11 IgG expression vector. Chimeric pIC11 light chain contains cloned
CC variable light chain (VL) and human kappa light chain constant region
CC (CL).
XX
SQ Sequence 125 AA;
 Query Match 100.0%; Score 48; DB 22; Length 125;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSSYPFT 9
 | | | | | | | | | |
Db 107 QORSSYPFT 115

RESULT 13
ID AAB82702
XX AAB82702 standard; Protein; 125 AA.
AC AAB82702;
XX
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1c11 light chain variable region.
XX
KW IMC-1c11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..125
FT /label= Mature_protein
FT Region 43..52
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT Region 68..74
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT Region 107..115
FT /label= CDR-L3
FT /note= "complementarity determining region 3"
XX
PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US02839.
XX
PR 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Kerbel R;
XX
DR WPI; 2001-514531/56.
DR N-PSDB; AAB26414.
XX
PT Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -

XX PS Disclosure; Fig 1; 42pp; English.

XX CC The present sequence is that of the light chain variable region of

XX CC IMC-1c11, a mouse-human chimeric antibody that has vascular

XX CC endothelial growth factor (VEGF) antagonist activity. The antibody,

XX CC or a fragment of it, can be used as an anti-angiogenic molecule,

XX CC together with a chemotherapeutic acid, for the treatment of an

XX CC angiogenic dependent condition in a mammal, especially a human.

XX CC The invention relates generally to a method of treating or

XX CC controlling an angiogenic dependent condition by administering an

XX CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a

XX CC regression or arrest of the condition while minimising or

XX CC preventing significant toxicity of the chemotherapeutic agent.

XX CC The anti-angiogenic molecule inhibits or blocks the action of a

XX CC vascular endothelium survival factor such as VEGF or its receptor,

XX CC and is especially IMC-1c11. Conditions that can be treated include

XX CC a neoplasm, a collagen-vascular disease or an autoimmune disease,

XX CC especially a solid tumour, including breast carcinoma, lung

XX CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,

XX CC ovarian carcinoma, neuroblastoma, central nervous system tumour,

XX CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX SQ Sequence 125 AA;

Query Match 100.0%; Score 48; DB 22; Length 125;

Best Local Similarity 100.0%; Pred. No. 0.086;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSSYPPT 9

Db 107 QQRSSYPPT 115

RESULT 14

ID AAU74420 standard; Protein; 238 AA.

XX AC AAU74420;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein, single chain variable fragment version #2.

XX KW Antigen-binding protein; single chain variable fragment; scFv; antigen;

XX KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

XX KW vascular endothelial growth factor receptor; VEGF;

XX KW cell proliferation inhibitor.

XX OS Mus sp.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Region 1..117

XX FT /label= VH

XX FT /note= "Heavy chain variable domain. Specifically

XX FT claimed in claim 61"

XX FT Region 118..132

XX FT /label= Linker

XX FT /note= "15 amino acid linker joins the VH and VL

XX FT regions of the single chain variable fragment

XX FT protein. Encoded by AAS20285"

XX FT Region 133..238

XX FT /label= VL

XX FT /note= "Light chain variable domain. Specifically

XX FT claimed in claim 61"

XX PN WO200190192-A2.

XX XX 29-NOV-2001.

XX PD 24-MAY-2001; 2001WO-US16924.

XX PF

XX XX

PR 24-MAY-2000; 2000US-206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX PA

XX XX Zhu Z;

XX PI WPI; 2002-106189/14.

XX DR

XX XX

XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing

XX PT tumour growth and for inhibiting angiogenesis, comprises a complex of

XX PT two polypeptides and two second polypeptides

XX PS Claim 63; Page 62-63; 64pp; English.

XX CC The invention describes an antigen-binding protein (I) comprising a

XX CC complex of two polypeptides (P1) and two second polypeptides (P2) which

XX CC are stably associated in an immunoglobulin like complex. P1 has an

XX CC antigen-binding site located to the N terminus of immunoglobulin (Ig)

XX CC light chain constant domain (CL domain), and P2 has an antigen-binding

XX CC site located to the N terminus of the CH1 domain. (I) is useful for:

XX CC neutralising the activation of a vascular endothelial growth factor

XX CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

XX CC reducing endothelial cell proliferation; inhibiting VEGF induced

XX CC migration of human leukaemia cells; blocking interaction of a protein and

XX CC its ligand; promoting interactions between immune cells and target cells;

XX CC and in vivo and in vitro for investigative, diagnostic or treatment

XX CC methods. The design of (I) provides for efficient production so that

XX CC substantially all of the antigen-binding proteins produced are assembled

XX CC in the desired configuration. (I) is bivalent and bispecific, homogenous

XX CC and in tetrameric form. The heavy chain constant domains which constitute

XX CC the Fc region (e.g., CH2 and CH3 for an Ig molecule) of a natural

XX CC antibody and which provide other antibody functions can be present. There

XX CC is no requirement for processing in vitro to obtain the complete product.

XX CC This is the amino acid sequence of a single chain variable fragment

XX CC (scFv), an engineered protein containing a variable light and variable

XX CC heavy domain on one polypeptide, described in the method of the

XX CC invention.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 48; DB 23; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSSYPPT 9

Db 220 QQRSSYPPT 228

RESULT 15

AAU74419

ID AAU74419 standard; Protein; 240 AA.

XX AC AAU74419;

XX DT 26-MAR-2002 (first entry)

XX DE Antigen-binding protein, single chain variable fragment version #1.

XX KW Antigen-binding protein; single chain variable fragment; scFv; antigen;

XX KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;

XX KW vascular endothelial growth factor receptor; VEGF;

XX KW cell proliferation inhibitor.

XX OS Mus sp.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Region 1..117

XX FT /label= VH

XX FT /note= "Heavy chain variable domain. Specifically

XX FT claimed in claim 57"

XX FT Region 118..132


```

FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT
FT Region 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
XX WO200190192-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
XX
XX 24-MAY-2000; 2000US-206749P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2002-106189/14.
XX
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
XX tumour growth and for inhibiting angiogenesis, comprises a complex of
XX two polypeptides and two second polypeptides
XX
XX Claim 63; Page 62; 64pp; English.
XX
XX The invention describes an antigen-binding protein (I) comprising a
XX complex of two polypeptides (P1) and two second polypeptides (P2) which
XX are stably associated in an immunoglobulin like complex. P1 has an
XX antigen-binding site located to the N terminus of immunoglobulin (Ig)
XX light chain constant domain (CL domain), and P2 has an antigen-binding
XX site located to the N terminus of the CH1 domain. (I) is useful for:
XX neutralising the activation of a vascular endothelial growth factor
XX (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
XX reducing endothelial cell proliferation; inhibiting VEGF induced
XX migration of human leukaemia cells; blocking interaction of a protein and
XX its ligand; promoting interactions between immune cells and target cells;
XX and in vivo and in vitro for investigative, diagnostic or treatment
XX methods. The design of (I) provides for efficient production so that
XX substantially all of the antigen-binding proteins produced are assembled
XX in the desired configuration. (I) is bivalent and bispecific, homogeneous
XX and in tetrameric form. The heavy chain constant domains which constitute
XX the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
XX antibody and which provide other antibody functions can be present. There
XX is no requirement for processing in vitro to obtain the complete product.
XX This is the amino acid sequence of a single chain variable fragment
XX (scfv), an engineered protein containing a variable light and variable
XX heavy domain on one polypeptide, described in the method of the
XX invention.
XX
SQ Sequence 240 AA;
Query Match 100.0%; Score 48; DB 23; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSSYPFT 9
Db 220 QQRSSYPFT 228
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Job time : 4.8314 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 62.8081 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVRLQSGAELVGSASVKL.....AAYGDYEGYQGCTTIVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	117	AAE13143	Humanised antibody
2	631	100.0	117	AAE13143	VEGF antagonist an
3	631	100.0	117	AAU74417	Antigen-binding pr
4	631	100.0	136	AAE13143	VEGF antagonist an
5	631	100.0	238	AAU74420	Antigen-binding pr
6	624	98.9	117	AAU72335	Variable heavy cha
7	624	98.9	117	AAU74412	Antigen-binding pr
8	624	98.9	240	AAU74419	Antigen-binding pr
9	619	98.1	136	AAE13145	Chimeric p1c11 hea
10	558.5	88.5	535	AAW28491	Human p53 protein

11	558.5	88.5	535	18	AAW28492	Human p53 protein
12	554.5	87.9	116	21	AAV70787	Murine anti-p53 mo
13	553.5	87.7	243	19	AAW60769	Single chain antib
14	536.5	85.0	112	20	AAW89173	Anti-p53 monoclonal
15	536.5	85.0	118	18	AAW01586	Lead binding MAB 1
16	517.5	82.0	270	16	AAW75719	MFE-23 antibody.
17	517.5	82.0	556	22	AAU97935	ScFv-rearranged ca
18	517.5	82.0	556	22	AAU80040	Anti-carcinoembryo
19	511.5	81.1	124	15	AAW60566	Single chain antib
20	511.5	81.1	249	19	AAW60770	Single chain antib
21	511.5	81.1	553	18	AAW11508	H22-anti-CEA antib
22	511.5	81.1	553	20	AAW73223	Bispecific single
23	511.5	81.1	553	22	AAW85455	Bispecific single
24	511.5	81.1	553	22	AAW61960	Anti-carcinoembryo
25	506.5	80.3	124	15	AAW60565	Anti-carcinoembryo
26	505.5	80.1	116	13	AAW24807	RSV19 VH. Mus mus
27	504.5	80.0	116	14	AAW42804	RSV19 heavy chain
28	503.5	79.8	124	20	AAW39528	Murine COL1 VH cha
29	503.5	79.8	124	23	AAW76632	Murine Col-1(CEA a
30	502.5	79.6	120	18	AAW41387	Anti-CEA antibody
31	502.5	79.6	255	18	AAW41394	Chimeric anti-CEA
32	502.5	79.6	281	20	AAW82744	Fusion protein PIC
33	502.5	79.6	642	20	AAW82741	806.077 heavy chal
34	502.5	79.6	666	20	AAW82745	Fusion protein (80
35	501.5	79.5	116	14	AAW42802	RSV19 heavy chain
36	495	78.4	119	12	AAW41394	H3 region of MAB T
37	495	78.4	119	19	AAW48758	TAL antibody VH ch
38	494	78.3	119	12	AAW41395	Modified H3 region
39	488	77.3	140	12	AAW11384	Variable gamma hea
40	487.5	77.3	258	23	ABB05962	Monoclonal antibod
41	487.5	77.3	258	23	ABB05990	Mouse monoclonal a
42	487.5	77.3	258	23	ABB05994	Mouse and human ch
43	487.5	77.3	287	23	ABB05982	Monoclonal antibody
44	485.5	76.9	120	16	AAW79889	Anti-EGFR antibody
45	482.5	76.5	136	22	AAW35290	Murine FSCA antibo

ALIGNMENTS

RESULT 1

AAE13143
ID AAE13143 standard; Protein; 117 AA.

AC AAE13143;

DT 28-JAN-2002 (first entry)

Humanised antibody heavy chain fragment.

Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
human; chimeric.

OS Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX WO200174296-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI; 2001-662942/76.

DR N-PSDB; AAD21669.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
XX Claim 8; Page 15; 68pp; English.
XX
XX The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain fragment used in the exemplification of the
CC invention.
XX
XX Sequence 117 AA;
XX
Query Match 100.0%; Score 631; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWYKQRPQGLEWIGWIDPENGSDY 60
Db 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWYKQRPQGLEWIGWIDPENGSDY 60
QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDTAVYCNAYYGDYEGYWGQGTTVTVSS 117
Db 61 APKFOGKATMTADSSNTAYLQLSSLTSEDTAVYCNAYYGDYEGYWGQGTTVTVSS 117
RESULT 2
AAB82709
ID AAB82709 standard; Protein; 117 AA.
XX
AC AAB82709;
XX
XX 15-OCT-2001 (first entry)
XX
XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
FH 26..35
FT /label= CDR-H1
FT /note= "complementarity determining region 1"
FT 50..66
FT /label= CDR-H2
FT /note= "complementarity determining region 2"
FT 99..106
FT /label= CDR-H3
FT /note= "complementarity determining region 3"
XX
XX WO200154723-A1.
XX
XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-0502839.

XX 28-JAN-2000; 2000US-0178791.
PR 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Kerbel R;
XX
XX WPI; 2001-514531/56.
DR N-PSDB; AAH26405.
XX
XX Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent -
XX
XX Disclosure; Page 38; 42pp; English.
XX
XX The present sequence is that of the heavy chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
XX Sequence 117 AA;
XX
Query Match 100.0%; Score 631; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWYKQRPQGLEWIGWIDPENGSDY 60
Db 1 QVKLQSGAELVGSASVKLSCTTSGFNKIDFYMHVWYKQRPQGLEWIGWIDPENGSDY 60
QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDTAVYCNAYYGDYEGYWGQGTTVTVSS 117
Db 61 APKFOGKATMTADSSNTAYLQLSSLTSEDTAVYCNAYYGDYEGYWGQGTTVTVSS 117
RESULT 3
AAU74417
ID AAU74417 standard; peptide; 117 AA.
XX
AC AAU74417;
XX
XX 26-MAR-2002 (first entry)
XX
XX Antigen-binding protein heavy chain variable domain (VH) #2.
XX
XX Antigen-binding protein; antibody heavy chain variable domain;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
XX Mus sp.
OS
XX WO200190192-A2.
PN
XX

PD 29-NOV-2001.
XX
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
XX PR 24-MAY-2000; 2000US-206749P.
XX
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX
XX PI Zhu Z;
XX
XX DR WPI; 2002-106189/14.
XX DR N-PSDB; AAS20288.
XX
XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing
XX PT tumour growth and for inhibiting angiogenesis, comprises a complex of
XX PT two polypeptides and two second polypeptides
XX
XX PS Claim 61; Page 60; 64pp; English.
XX
XX CC The invention describes an antigen-binding protein (I) comprising a
XX CC complex of two polypeptides (P1) and two second polypeptides (P2) which
XX CC are stably associated in an immunoglobulin like complex. P1 has an
XX CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
XX CC light chain constant domain (C1 domain), and P2 has an antigen-binding
XX CC site located to the N terminus of the C1 domain. (I) is useful for:
XX CC neutralising the activation of a vascular endothelial growth factor
XX CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
XX CC reducing endothelial cell proliferation; inhibiting VEGF induced
XX CC migration of human leukaemia cells; blocking interaction of a protein and
XX CC its ligand; promoting interactions between immune cells and target cells;
XX CC and in vivo and in vitro for investigative, diagnostic or treatment
XX CC methods. The design of (I) provides for efficient production so that
XX CC substantially all of the antigen-binding proteins produced are assembled
XX CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
XX CC and in tetrameric form. The heavy chain constant domains which constitute
XX CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
XX CC antibody and which provide other antibody functions can be present. There
XX CC is no requirement for processing in vitro to obtain the complete product.
XX CC This sequence represents a heavy chain variable domain (VH) incorporated
XX CC into Fv, an engineered protein containing a heavy chain variable domain
XX CC and a light chain variable domain in one polypeptide chain, described in
XX CC the method of the invention.
XX
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 631; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGSDSY 60
DB 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGSDSY 60

QY 61 APKFGKATMTADSSNTAYLQSLTSDTAVYYCNAYGYDEYWGQGTFTVYSS 117
DB 61 APKFGKATMTADSSNTAYLQSLTSDTAVYYCNAYGYDEYWGQGTFTVYSS 117

RESULT 4
AAB82701
ID AAB82701 standard; Protein; 136 AA.
XX
XX AC AAB82701;
XX
XX DT 15-OCT-2001 (first entry)
XX
XX DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.
XX
XX KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;

KW glioblastoma multiforme; melanoma; therapy; heavy chain.
XX
XX OS Chimeric - Mus sp.
XX OS Chimeric - Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein 20..136
XX FT Region 45..54
XX FT /label= CDR-H1
XX FT /note= "complementarity determining region 1"
XX FT /label= CDR-H2
XX FT /note= "complementarity determining region 2"
XX FT /label= CDR-H3
XX FT /note= "complementarity determining region 3"
XX
XX PN WO200154723-A1.
XX PD 02-AUG-2001.
XX
XX PF 29-JAN-2001; 2001WO-US02839.
XX PF 28-JAN-2000; 2000US-0178791.
XX PF 31-MAR-2000; 2000US-0539692.
XX PR (SUNN-) SUNNYBROOK HEALTH SCI CENT.
XX PR (IMCL-) IMCLONE SYSTEMS INC.
XX
XX PI Kerbel R;
XX
XX DR WPI; 2001-514531/56.
XX DR N-PSDB; RAH26413.
XX
XX PT Treating or controlling an angiogenic dependent condition (e.g. a
XX PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
XX PT administering a combination of an antiangiogenic molecule and a
XX PT chemotherapeutic agent -
XX
XX PS Disclosure; Fig 1; 42pp; English.
XX
XX CC The present sequence is that of the heavy chain variable region of
XX CC IMC-1C11, a mouse-human chimeric antibody that has vascular
XX CC endothelial growth factor (VEGF) antagonist activity. The antibody,
XX CC or a fragment of it, can be used as an anti-angiogenic molecule,
XX CC together with a chemotherapeutic acid, for the treatment of an
XX CC angiogenic dependent condition in a mammal, especially a human.
XX CC The invention relates generally to a method of treating or
XX CC controlling an angiogenic dependent condition by administering an
XX CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
XX CC regression or arrest of the condition while minimising or
XX CC preventing significant toxicity of the chemotherapeutic agent.
XX CC The anti-angiogenic molecule inhibits or blocks the action of a
XX CC vascular endothelium survival factor such as VEGF or its receptor,
XX CC and is especially IMC-1C11. Conditions that can be treated include
XX CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
XX CC especially a solid tumour, including breast carcinoma, lung
XX CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
XX CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
XX CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
XX SQ Sequence 136 AA;

Query Match 100.0%; Score 631; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGSDSY 60
DB 20 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGSDSY 79

QY 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTTVTVSS 117
 |||||
 Db 80 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTTVTVSS 136
 |||||
 RESULT 5
 AAU74420
 ID AAU74420 standard; Protein; 238 AA.
 XX
 AC AAU74420;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Antigen-binding protein, single chain variable fragment version #2.
 XX
 KW Antigen-binding protein; single chain variable fragment; svFv; antigen;
 KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 KW cell proliferation inhibitor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT 1..117
 FT /label= VH
 FT /note= "Heavy chain variable domain. Specifically
 FT claimed in claim 61"
 FT
 FT Region
 FT 118..132
 FT /label= Linker
 FT /note= "15 amino acid linker joins the VH and VL
 FT regions of the single chain variable fragment
 FT protein. Encoded by AAS20285"
 FT
 FT Region
 FT 133..238
 FT /label= VL
 FT /note= "Light chain variable domain. Specifically
 FT claimed in claim 61"
 FT
 FT WO200190192-A2.
 XX
 PN 29-NOV-2001.
 XX
 XX 24-MAY-2001; 2001WO-US16924.
 XX
 XX 24-MAY-2000; 2000US-206749P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 XX Zhu Z;
 XX
 XX WPI; 2002-106189/14.
 XX
 XX New bispecific immunoglobulin-like antigen-binding protein for reducing
 XX tumour growth and for inhibiting angiogenesis, comprises a complex of
 XX two polypeptides and two second polypeptides
 XX
 XX Claim 63; Page 62-63; 64pp; English.
 XX
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled

CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and tetrameric form. The heavy chain constant domains which constitute
 CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This is the amino acid sequence of a single chain variable fragment
 CC (scFv), an engineered protein containing a variable light and variable
 CC heavy domain on one polypeptide, described in the method of the
 CC invention.

XX Sequence 238 AA;

Query Match 100.0%; Score 631; DB 23; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.8e-47;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAELVGSASVKLSCTTSFNIKDFYMHVYKQRPQGLEWIGWIDPENGSDSY 60
 |||||
 Db 1 QVQLQSGAELVGSASVKLSCTTSFNIKDFYMHVYKQRPQGLEWIGWIDPENGSDSY 60
 |||||
 QY 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTTVTVSS 117
 |||||
 Db 61 APKFGKATMTADSSNTAYLQLSLTSEDVAVYCNAYYGDYEGYWGQGTTVTVSS 117
 |||||

RESULT 6

AA97235
 ID AA97235 standard; Protein; 117 AA.

XX
 AC AA97235;

XX 19-DEC-2000 (first entry)

XX Variable heavy chain fragment of anti-SI(KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR;

KW VEGF; vascular endothelial growth factor; KDR;

KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diabody;

KW glioblastoma multiforme; hemangioblastoma; AIDS;

KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;

KW acquired immune deficiency syndrome; AIDS; human.

XX Homo sapiens.

OS Synthetic.

XX WO2000044777-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US02180.

XX 29-JAN-1999; 99US-0117726.

XX 29-JAN-1999; 99US-0240736.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z, Witte L;

XX WPI; 2000-505966/45.

XX N-PSDB; AAA53767.

XX Novel immunoglobulin molecules binding kinase insert domain-containing

XX receptor with the same affinity as vascular endothelial growth factor,

XX used to reduce tumour growth

XX Claim 4; Page 50-51; 55pp; English.

XX New immunoglobulin molecules are described that bind kinase insert

XX domain-containing receptor (KDR) with a comparable affinity to human

XX vascular endothelial growth factor (VEGF). The antibodies neutralise

XX KDR activation. The immunoglobulin may be a multivalent single

XX chain antibody, a monovalent single chain antibody, a diabody, a

CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
SQ Sequence 117 AA;
Query Match 98.9%; Score 624; DB 21; Length 117;
Best Local Similarity 99.1%; Pred. No. 5.3e-47;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QVKLQSGAELVGGASVYKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 1 QVKLQSGAELVGGASVYKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Qy 61 APKFGKATMTADSSNTAYLQLSLTSDTAVYYCNAYYGDYEGYWGQGTIVTVSS 117
Db 61 APKFGKATMTADSSNTAYLQLSLTSDTAVYYCNAYYGDYEGYWGQGTIVTVSS 117
RESULT 7
AAU74412
ID AAU74412 standard; peptide: 117 AA.
XX
AC AAU74412;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein heavy chain variable domain (VH) #1.
XX
KW Antigen-binding protein; antibody heavy chain variable domain;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
DR N-PSDB; AAS20283.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 57; Page 57; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced

CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 117 AA;
Query Match 98.9%; Score 624; DB 23; Length 117;
Best Local Similarity 99.1%; Pred. No. 5.3e-47;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QVKLQSGAELVGGASVYKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Db 1 QVKLQSGAELVGGASVYKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGDSY 60
Qy 61 APKFGKATMTADSSNTAYLQLSLTSDTAVYYCNAYYGDYEGYWGQGTIVTVSS 117
Db 61 APKFGKATMTADSSNTAYLQLSLTSDTAVYYCNAYYGDYEGYWGQGTIVTVSS 117
RESULT 8
AAU74419
ID AAU74419 standard; Protein: 240 AA.
XX
AC AAU74419;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein, single chain variable fragment version #1.
XX
KW Antigen-binding protein; single chain variable fragment; scFv; antigen;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key
FH Region 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"
FT Region 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"
FT Region 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX

PI Zhu Z;
 XX WPI: 2002-106189/14.
 XX
 XX New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides -
 XX
 XX Claim 63: Page 62; 64pp; English.
 XX
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody (and which provide other antibody functions) can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This is the amino acid sequence of a single chain variable fragment
 CC (scFv), an engineered protein containing a variable light and variable
 CC heavy domain on one polypeptide, described in the method of the
 CC invention.
 XX
 SQ Sequence 240 AA;
 Query Match 98.9%; Score 624; DB 23; Length 240;
 Best Local Similarity 99.1%; Pred. No. 1.1e-46;
 Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKQRPQGLEWIGWIDPENGSDSY 60
 DB 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKQRPQGLEWIGWIDPENGSDSY 60
 QY 61 APKFGKATMTADSSNTAYLQLSSLTSETAVYCNAYGDEYEGWGQGTTVTVSS 117
 DB 61 APKFGKATMTADSSNTAYLQLSSLTSETAVYCNAYGDEYEGWGQGTTVTVSS 117
 RESULT 9
 ID AAE13145 standard; Protein; 136 AA.
 AC AAE13145;
 XX
 XX 28-JAN-2002 (first entry)
 DE Chimeric p1c11 heavy chain fragment.
 XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytosstatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
 KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
 KW human; p1c11 vector.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Unidentified.
 XX
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /label= Leader_peptide
 FT Protein 20..136
 FT /note= "Mature chimeric p1c11 heavy chain fragment"
 FT Region 45..54

FT /label= CDR_H1
 FT 69..85
 FT /label= CDR_H2
 FT Misc-difference 84
 FT /note= "Residue 'O' is present at this location in the
 FT sequence shown in fig-11 of the specification"
 FT Misc-difference 101
 FT /note= "Residue 'O' is present at this location in the
 FT sequence shown in fig-11 of the specification"
 FT 119..125
 FT /label= CDR_H3
 FT
 XX WO200174296-A2.
 PN 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10504.
 PR 31-MAR-2000; 2000US-0540770.
 XX (IMCL-) IMCLONE SYSTEMS INC.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Witte L, Rafii S;
 XX WPI: 2001-662942/76.
 DR N-PSDB; AAD21682.
 XX
 XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with
 PT an antagonist of a vascular endothelial growth factor receptor -
 XX
 XX Example 3; Fig 11; 68pp; English.
 XX
 CC The invention relates to a method for inhibiting the growth of non-solid
 CC tumour cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to
 CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
 CC p1c11 heavy chain fragment which is used for the construction of chimeric
 CC p1c11 IgG expression vector. Chimeric p1c11 heavy chain contains cloned
 CC variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
 CC domain (CH).
 XX
 SQ Sequence 136 AA;
 Query Match 98.1%; Score 619; DB 22; Length 136;
 Best Local Similarity 98.3%; Pred. No. 1.7e-46;
 Matches 115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKQRPQGLEWIGWIDPENGSDSY 60
 DB 20 QVKLQSGAELVGSASVKLSCTTSGFNKDFYMHVWVKQRPQGLEWIGWIDPENGSDSY 79
 QY 61 APKFGKATMTADSSNTAYLQLSSLTSETAVYCNAYGDEYEGWGQGTTVTVSS 117
 DB 80 APKFGKATMTADSSNTAYLQLSSLTSETAVYCNAYGDEYEGWGQGTTVTVSS 136
 RESULT 10
 ID AAW28491 standard; Protein; 535 AA.
 XX
 XX AAW28491;
 XX 25-NOV-1997 (first entry)
 DT

XX DE Human p53 protein variant S-325 encoded by pEC176.
XX KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
XX KW substitution; replacement; transactivation; viral protein VP16; HSV;
XX KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
XX KW tumour suppression; apoptosis; single chain antibody variable domain.
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Herpes simplex virus.
XX OS Synthetic.
XX PN WO9704092-A1.
XX PD 06-FEB-1997.
XX PF 17-JUL-1996; 96WO-FR01111.
XX PR 19-JUL-1995; 95FR-0008729.
XX PA (RHON) RHONE POULENC RORER SA.
XX PI Bracco L, Conseiller E;
XX DR WPI; 1997-132633/12.
XX DR N-PSDB; AAT86221.
XX PF New p53 variants e.g. with oligomerisation domain replaced by
XX PT leucine zipper - useful for treating hyper-proliferative disorders,
XX PT esp. cancer and restenosis
XX PS Claim 36; Pages 88-90; 133pp; French.
XX CC Claimed variants of protein p53 have at least part of the
XX CC oligomerisation domain deleted and replaced by a leucine zipper
XX CC domain. The mutants preferably also have at least part of the p53
XX CC transactivating domain (amino acids 1-74) deleted and replaced by
XX CC the transactivating domain (TD) from herpes simplex virus viral
XX CC protein VP16 (amino acids 411-490) or by a protein domain able to
XX CC bind selectively to a transactivator, especially a single-chain
XX CC antibody variable domain (ScFv). The present sequence is that of
XX CC a specifically claimed p53 variant designated S-325 and comprising
XX CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a
XX CC leucine zipper domain at the C-terminal. The p53 variants are
XX CC more active and more stable tumour suppressors and apoptosis-inducing
XX CC agents than wild-type p53 and are active where the wild-type protein
XX CC is not, i.e. they are not inactivated by dominant negative or oncogenic
XX CC mutants, nor by other cellular proteins (because the leucine zipper
XX CC domain prevents formation of inactive mixed oligomers).
XX SQ Sequence 535 AA;
Query Match 88.5%; Score 558.5; DB 18; Length 535;
Best Local Similarity 88.9%; Pred. No. 1.3e-40;
Matches 104; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVGSGSVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDSY 60
Db 3 QVQLQESGAELVGSGSVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDTY 62
QY 61 APKFOGKATMTADSSNTAYLQSLSSDTAVYICNAVYGYEGYWGOGTTVTYSS 117
Db 63 APKFOGKATMTADSSNTAYLQSLSSDTAVYICNAVYICN-FYGDALDYWGOGTTVTYSS 118
RESULT 11
AAW28492
ID AAW28492 standard; Protein; 535 AA.
XX AAW28492;
XX AC AAW28492;
XX DT 25-NOV-1997 (first entry)
XX

DE Human p53 protein variant S-325H.
XX KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
XX KW substitution; replacement; transactivation; viral protein VP16; HSV;
XX KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
XX KW tumour suppression; apoptosis; single chain antibody variable domain.
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Herpes simplex virus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 361 /note= "Arg residue at position 182 of wild-type
XX FT p53 has been mutated to His"
XX PN WO9704092-A1.
XX PD 06-FEB-1997.
XX PF 17-JUL-1996; 96WO-FR01111.
XX PR 19-JUL-1995; 95FR-0008729.
XX PA (RHON) RHONE POULENC RORER SA.
XX PI Bracco L, Conseiller E;
XX DR WPI; 1997-132633/12.
XX PT New p53 variants e.g. with oligomerisation domain replaced by
XX PT leucine zipper - useful for treating hyper-proliferative disorders,
XX PT esp. cancer and restenosis
XX PS Claim 36; Page -; 133pp; French.
XX CC Claimed variants of protein p53 have at least part of the
XX CC oligomerisation domain deleted and replaced by a leucine zipper
XX CC domain. The mutants preferably also have at least part of the p53
XX CC transactivating domain (amino acids 1-74) deleted and replaced by
XX CC the transactivating domain (TD) from herpes simplex virus viral
XX CC protein VP16 (amino acids 411-490) or by a protein domain able to
XX CC bind selectively to a transactivator, especially a single-chain
XX CC antibody variable domain (ScFv). The present sequence is that of
XX CC a specifically claimed p53 variant designated S-325H and comprising
XX CC a ScFv domain, amino acids 75-325 of human wild-type p53 (but with
XX CC Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
XX CC The p53 variants are more active and more stable tumour suppressors
XX CC and apoptosis-inducing agents than wild-type p53 and are active where
XX CC the wild-type protein is not, i.e. they are not inactivated by dominant
XX CC negative or oncogenic mutants, nor by other cellular proteins (because
XX CC the leucine zipper domain prevents formation of inactive mixed
XX CC oligomers).
XX CC (Note: this sequence does not appear in the specification and has
XX CC been produced by modifying the given sequence of variant V-325).
XX SQ Sequence 535 AA;
Query Match 88.5%; Score 558.5; DB 18; Length 535;
Best Local Similarity 88.9%; Pred. No. 1.3e-40;
Matches 104; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
QY 1 QVKLQSGAELVGSGSVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDSY 60
Db 3 QVQLQESGAELVGSGSVKLSCTTSGFNKIDFYMHVWVKORPEQGLEWIGWIDPENGDTY 62
QY 61 APKFOGKATMTADSSNTAYLQSLSSDTAVYICNAVYGYEGYWGOGTTVTYSS 117
Db 63 APKFOGKATMTADSSNTAYLQSLSSDTAVYICNAVYICN-FYGDALDYWGOGTTVTYSS 118
RESULT 12
AAW70787

AAV70787 standard; Protein; 116 AA.

AAV70787; (first entry)

31-JUL-2000 (first entry)

Murine anti-p53 monoclonal antibody PAB-421 heavy chain variable region.

Murine; p53 protein; monoclonal antibody; PAB-421; DNA-binding domain; dermatological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; heavy chain variable region; VH; complementarity determining region; CDR.

Mus sp.

Key Location/Qualifiers

Region 26..35

Region /label= CDR

Region /note= "Complementarity determining region"

Region 50..66

Region /label= CDR

Region /note= "Complementarity determining region"

Region 99..105

Region /label= CDR

Region /note= "Complementarity determining region"

WO200023082-A1.

27-APR-2000.

19-OCT-1999; 99WO-US24443.

19-OCT-1998; 98US-0104816.

(VEDA) VEDA RES & DEV CO LTD.

Cohen IR, Rotter V, Erez-Alon N, Herkel J;

WPI; 2000-339512/29.

Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or fragments of p53.

Claim 78; Fig 9; 87pp; English.

The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the C-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a heavy chain variable region of monoclonal antibody PAB-421 which is specific to the C-terminal DNA-binding domain of murine p53 protein. PAB-421 antibody and peptides based on complementarity determining regions of light and heavy chain variable regions of the antibody, are examples of active compounds useful in the diagnosis, prevention and treatment of SLE in humans.

Sequence 116 AA;

Query Match 87.9%; Score 554.5; DB 21; Length 116;

Best Local Similarity 88.9%; Pred. No. 5.9e-41;

Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVGSGASVKLSCTTSGFNKDFYHHVKKRPEQGLEWIGWIDPENGSDY 60

Db 1 QVKLQSGAELVRSASVKLSCTASGFNIDYHHVKKRPEQGLEWIGWIDPENGDEY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYWGQGTTVTVSS 117

Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYWGQGTTVTVSS 116

RESULT 13

AAW60769

ID AAW60769 standard; Protein; 243 AA.

XX AAW60769;

AC AAW60769;

XX 08-SEP-1998 (first entry)

DT 08-SEP-1998 (first entry)

DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.

XX Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation; regulatory domain; p53 mutant; H273; W248; G281;

KW p53-dependent trans-activating activity; restoration;

KW tumour-suppressing activity; tumour cell; treatment;

XX hyper-proliferation; cancer; re-stenosis; ss.

XX Mus sp.

OS WO9818825-A1.

XX 07-MAY-1998.

PD 27-OCT-1997; 97WO-FR01921.

XX 29-OCT-1996; 96FR-0013176.

XX (RHON) RHONE-POULENC RORER SA.

XX Debussche L, Bracco L;

PI WPI; 1998-272140/24.

XX N-PSDB; AAV36236.

DR Restoring p53-dependent trans-activating activity to cell containing mutant p53 - by delivering single-chain antibody specific for the mutant, particularly for treatment of tumours

PT Claim 5; Page 31; 54pp; French.

XX The present sequence represents a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53-dependent trans-activating activity is restored. ScFv 421 is specific for p53-mutants that have lost tumour-suppressing activity and are present in tumour cells. It is particularly used to treat hyper-proliferation associated with these mutants (e.g. cancer and re-stenosis) but may also be used in vitro for studying mechanisms of activity of p53 or its mutant and to purify or detect p53.

XX Sequence 243 AA;

Query Match 87.7%; Score 553.5; DB 19; Length 243;

Best Local Similarity 88.9%; Pred. No. 1.5e-40;

Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 QVKLQSGAELVGSGASVKLSCTTSGFNKDFYHHVKKRPEQGLEWIGWIDPENGSDY 60

Db 1 QVKLQSGAELVRSASVKLSCTASGFNIDYHHVKKRPEQGLEWIGWIDPENGDEY 60

QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYWGQGTTVTVSS 117

Db 61 APKFGKATMTADSSNTAYLQLSSLTSEDYAVYCNAYGYEGYWGQGTTVTVSS 116

RESULT 14

AAW89173

ID AAW89173 standard; peptide; 112 AA.

XX AAW89173;

AC AAW89173;

XX 25-MAR-1999 (first entry)

DT

```

XX DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
XX DE
XX DE Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.
KW KW
XX OS Synthetic.
XX OS
XX PN WO9856416-A1.
XX PN
XX PD 17-DEC-1998.
XX PD
XX PF 09-JUN-1998; 98WO-IL00266.
XX PF
XX PR 09-JUN-1997; 97IL-0121041.
XX PR
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PA
XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
PI Wolkowicz R;
XX PI
XX DR WPI; 1999-070296/06.
XX DR
XX XX Use of a monoclonal antibody to a tumour-associated antigen - to
PT induce anti-tumour immunity or elicit an increased immune response
PT to the antigen
XX PT
XX PS Example 3; Fig 3; 47pp; English.
XX PS
XX CC The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarity determining region) on the heavy or light chain of Mab
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of Mab, in a gene delivery vehicle. The present
CC sequence represents the variable heavy chain sequence from anti-p53 Mab
CC 421. Also described is a method for generating sequence-specific,
CC anti-DNA antibodies (Ab) by immunising a mammal with a Mab directed to a
CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
CC used to treat a wide variety of primary and metastatic cancers,
CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
CC to determine critical sequences in animal or plant breeding); to
CC identify bacteria and other parasites; to determine parentage; in
CC forensic science; to isolate specific genes for DNA vaccination; in gene
CC sequencing and cloning; also possibly for activation of selected
CC therapeutic genes in plants, animals and humans. (A) induce an effective
CC anti-tumour response without causing harm to the patient. The method
CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.
XX CC
XX SQ Sequence 112 AA;
XX SQ
Query Match 85.0%; Score 536.5; DB 20; Length 112;
Best Local Similarity 88.5%; Pred. No. 2.le-39;
Matches 100; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Qy 4 LQSGAELVSGASVKLSCTTSGFNKDFYMHVWQKRPQGLWIGWIDPENGSDYAPK 63
Db 1 LQSGAELVSGASVKLSCTTSGFNKDFYMHVWQKRPQGLWIGWIDPENGSDYAPK 60
Qy 64 FQKATMTADSSNTAYLQSLTSEDYAVYCNAY-YGDYEGYWGQGTVTYVS 116
Db 61 FQKATMTADTSSNTAYLQSLTSEDYAVYCNAY-FYGDALDYWGQGTVTYVS 112

RESULT 15
AAW01586
ID AAW01586 standard; Protein; 118 AA.
XX AC
XX AC AAW01586;
XX XX

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DT 22-AUG-1997 (first entry)
DE
XX DE Lead binding MAB 14G11 heavy chain variable region.
XX DE
XX KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.
XX KW
XX OS Mus musculus.
XX OS
XX PN WO9639518-A1.
XX PN
XX PD 12-DEC-1996.
XX PD
XX PF 05-JUN-1996; 96WO-US09258.
XX PF
XX PR 10-OCT-1995; 95US-0541373.
XX PR
XX PR 05-JUN-1995; 95US-0462798.
XX PR
XX PA (BION-) BIONEBRASKA INC.
XX PA
XX PI Lopez O, Murray PJ, Wylie DE;
XX PI
XX DR WPI; 1997-043140/04.
XX DR
XX DR N-PSDB; AAT58260.
XX DR
XX PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as
XX lead cations
XX PT
XX PS Claim 12; Page 75; 125pp; English.
XX PS
XX CC The present sequence represents the heavy chain variable region for
XX monoclonal antibody (MAB) 14G11, which immunoreacts with a lead cation.
XX The sequence was derived from RNA isolated from mouse hybridoma cells.
XX The protein can be used for binding heavy metals, such as lead cations.
XX It can be used for detecting, removing, adding or neutralising the
XX heavy metals in biological and inanimate systems. It can be used in
XX e.g. aqueous liquid systems, in biological or environmental systems or
XX in such compositions as perfumes, cosmetics, pharmaceuticals, health
XX care products, skin treatment products, pesticides, herbicides,
XX solvents used in the production of semi-conductor and integrated
XX circuit components and production materials for electronic components.
XX The products can provide for applications involving minute amounts of
XX specific heavy metals.
XX CC
XX SQ Sequence 118 AA;
XX SQ
Query Match 85.0%; Score 536.5; DB 18; Length 118;
Best Local Similarity 85.6%; Pred. No. 2.2e-39;
Matches 101; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWQKRPQGLWIGWIDPENGSDY 60
Db 1 EVQLQSGAELVSGASVKLSCTTSGFNKDFYMHVWQKRPQGLWIGWIDPENGDT 60
Qy 61 APKFGKATMTADSSNTAYLQSLTSEDYAVYCNAY-YGDYEGYWGQGTVTYVS 117
Db 61 DPKFGKATMTADTSSNTAYLQSLTSEDYAVYCNAY-PGYDDAMDYWGQGTSTYVS 118

Search completed: December 23, 2002, 07:25:10
Job time : 63.8081 secs

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 56.9031 seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-23

Perfect score: 549

Sequence: 1 DIELTQSPAINASPGKVT.....CQRRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	AAE13144	Humanised antibody
2	549	100.0	106	AAU74418	Antigen-binding pr
3	549	100.0	108	AAU97236	Variable light cha
4	549	100.0	108	AAAB82710	VEGF antagonist an
5	549	100.0	108	AAU74413	Antigen-binding pr
6	549	100.0	125	AAE13146	Chimeric p1C11 lig
7	549	100.0	125	AAAB82702	VEGF antagonist an
8	549	100.0	238	AAU74420	Antigen-binding pr
9	549	100.0	240	AAU74419	Antigen-binding pr
10	549	100.0	330	AAAB70842	SNV-env leader/hum

11	534	97.3	108	16	AAU79884	Anti-EGFR antibody
12	534	97.3	235	18	AAW41392	Chimeric anti-CEA
13	532	96.9	108	13	AAU21290	Murine VL kappa gr
14	532	96.9	108	18	AAW41388	Anti-CEA antibody
15	529	96.4	107	22	AAAB83159	Mouse ganglioside
16	529	96.4	129	15	AAAS3329	KM-796 and KM-750
17	529	96.4	129	20	AAU28385	Anti-GM2 light cha
18	529	96.4	129	20	AAU28357	Antibody chain use
19	527	96.0	256	22	AAAB82897	Anti-p53 common mu
20	527	96.0	258	22	AAAB82898	Anti-p53 common mu
21	526	95.8	107	22	AAAG3987	Amino acid sequenc
22	524	95.4	108	13	AAU21294	Murine VL kappa gr
23	523	95.3	236	20	AAU34096	Partial amino acid
24	523	95.3	270	16	AAU75719	MFE-23 antibody.
25	523	95.3	553	18	AAW11508	Single chain anti-
26	523	95.3	553	20	AAW73223	H22-anti-CEA antib
27	523	95.3	553	22	AAAB85455	Bispecific single
28	523	95.3	553	22	AAAB19660	Bispecific single
29	521	94.9	281	20	AAW82744	Fusion protein PIC
30	521	94.9	666	20	AAW82745	Fusion protein (80
31	519	94.5	109	23	AAU81278	Murine trkC antibo
32	519	94.5	556	22	AAU97935	scFv-rearranged ca
33	519	94.5	556	22	AAU80040	scFv-rearranged ca
34	516	94.4	105	17	AAW03182	Guy's 13 anti-Stre
35	516	94.0	106	13	AAU24105	Anti-Tac light cha
36	516	94.0	106	19	AAW58511	Anti-Tac light cha
37	516	94.0	106	22	AAAB69641	Protein SEQ ID NO:
38	516	94.0	106	22	AAAB69651	Murine anti-Tac an
39	516	94.0	128	10	AAU93150	Protein encoded by
40	516	94.0	239	21	AAAB12563	Anti-TAC sfv prote
41	516	94.0	239	22	AAAB36826	Anti-TAC sfv prote
42	516	94.0	599	19	AAW37132	Anti-Tac(Fv)-PE40
43	516	94.0	599	20	AAW95462	Anti-Tac(Fv)-PE40
44	516	94.0	599	21	AAU87477	Anti-Tac(Fv)-PE40
45	511	93.1	128	21	AAAB19639	Mouse monoclonal a

ALIGNMENTS

RESULT 1
AAE13144
ID AAE13144 standard; Protein; 106 AA.
XX
XX AAE13144;
AC
XX
XX 28-JAN-2002 (first entry)
DT
XX Humanised antibody light chain fragment.
DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain; myelocytic leukemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
XX WO200174296-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10504.
PF
XX 31-MAR-2000; 2000US-0540770.
PR
XX {IMCL-} IMCLONE SYSTEMS INC.
PA (CORR) CORNELL RES FOUND INC.
XX
XX Witte L, Rafii S;
PI
XX WPI; 2001-662942/76.
DR
XX N-PSDB; AAD21670.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
PS Claim 8; Page 16; 68pp; English.
XX
CC The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody light chain fragment used in the exemplification of the
CC invention.
XX
SQ Sequence 106 AA;
Query Match 100.0%; Score 549; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPAR 60
DB 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPAR 60
QY 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
RESULT 2
AAU74418
ID AAU74418 standard; peptide: 106 AA.
XX
AC AAU74418;
XX
DT 26-MAR-2002 (first entry)
XX
DE Antigen-binding protein light chain variable domain (VH) #2.
XX
KW Antigen-binding protein; antibody light chain variable domain;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
OS Mus sp.
XX
PN WO200190192-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US16924.
XX
PR 24-MAY-2000; 2000US-206749P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2002-106189/14.
XX
DR N-PSDB; AAU20289.
XX
PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX

PS Claim 61; Page 61; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a light chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 106 AA;
Query Match 100.0%; Score 549; DB 23; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPAR 60
DB 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPAR 60
QY 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
RESULT 3
AAU97236
ID AAU97236 standard; Protein; 108 AA.
XX
AC AAU97236;
XX
DT 19-DEC-2000 (first entry)
XX
DE Variable light chain fragment of anti-SI(KDR) antibody.
XX
KW Immunoglobulin; antibody; complementary determining region; CDR;
KW VEGF; vascular endothelial growth factor; KDR;
KW kinase insert domain containing receptor; multivalent; monovalent;
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200044777-A1.
XX
PD 03-AUG-2000.
XX
PD 28-JAN-2000; 2000WO-US02180.
XX
PF 29-JAN-1999; 99US-0117726.
XX
PR 29-JAN-1999; 99US-0240736.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX

PI Zhu Z, Witte L;
XX WPI; 2000-505966/45.
DR N-PSDB; AAA53768.
XX
XX Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
XX Claim 4; Page 51; 55pp; English.
XX
XX New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
XX
XX Sequence 108 AA;
SQ
Query Match 100.0%; Score 549; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR 60
Qy 61 FSGSGSGTYSILTSRMEADAATYCCQRRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTYSILTSRMEADAATYCCQRRSSYPFTFGSGTKLEIK 106
RESULT 4
AAB82710
ID AAB82710 standard; Protein; 108 AA.
XX
XX AAB82710;
AC
XX 15-OCT-2001 (first entry)
DT
XX VEGF antagonist antibody IMC-1C11 light chain variable region.
DE
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
FH 24..33
FT /label= CDR-L1
FT /note= "complementarity determining region 1"
FT 49..55
FT /label= CDR-L2
FT /note= "complementarity determining region 2"
FT 88..96
FT /label= CDR-L3
FT /note= "complementarity determining region 3"
XX

PN WO200154723-A1.
XX
PD 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US02839.
XX
XX 28-JAN-2000; 2000US-0178791.
PR
PR 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
PA (IMCL-) IMCLONE SYSTEMS INC.
PA
XX Kerbel R;
PI
XX WPI; 2001-514531/56.
DR N-PSDB; AAH26406.
XX
XX Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent
XX
XX Disclosure; Page 38-39; 42pp; English.
PS
XX The present sequence is that of the light chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.
CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.
CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 549; DB 22; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLASGVPAR 60
Qy 61 FSGSGSGTYSILTSRMEADAATYCCQRRSSYPFTFGSGTKLEIK 106
Db 61 FSGSGSGTYSILTSRMEADAATYCCQRRSSYPFTFGSGTKLEIK 106
RESULT 5
AAU74413
ID AAU74413 standard; peptide; 108 AA.
XX
XX AAU74413;
AC
XX 26-MAR-2002 (first entry)
DT
XX Antigen-binding protein light chain variable domain (VH) #1.
DE
XX Antigen-binding protein; antibody light chain variable domain;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.

XX Mus sp.
OS WO200190192-A2.
PN
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
XX
XX 24-MAY-2000; 2000US-206749P.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI: 2002-106189/14.
DR N-PSDB; AAS20284.
XX
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
XX Claim 57; Page 57; 64pp; English.
XX
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor;
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a light chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 549; DB 23; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSYNMHWFOQKPGTSPKLIWYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMSASPGKVTITCSASSSYNMHWFOQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
RESULT 6
AAEI3146
ID AAEI3146 standard; Protein; 125 AA.
XX
XX AAEI3146;
XX
XX 28-JAN-2002 (first entry)
XX
XX Chimeric pic11 light chain fragment.
XX

KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
KW human; p1C11 vector.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX
XX Key Location/Qualifiers
XX 1..19 /label= Leader_peptide
FT Peptide /label= Leader_peptide
FT Protein 20..125 /note= "Mature chimeric p1C11 light chain fragment"
FT Region 43..52 /label= CDR_L1
FT Region 58..74 /label= CDR_L2
FT Region 107..115 /label= CDR_L3
XX
XX WO200174296-A2.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US10504.
XX
XX 31-MAR-2000; 2000US-0540770.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (CORR) CORNELL RES FOUND INC.
PA
XX Witte L, Rafii S;
XX
XX WPI: 2001-662942/76.
DR N-PSDB; AAD21883.
XX
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
XX Example 3; Fig 11; 68pp; English.
XX
XX The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1C11 light chain fragment which is used for the construction of chimeric
CC p1C11 IgG expression vector. Chimeric p1C11 light chain contains cloned
CC variable light chain (VL) and human kappa light chain constant region
CC (CL).
XX
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 549; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.6e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTITCSASSSYNMHWFOQKPGTSPKLIWYSTSNLASGVPAR 60
DB 20 DIELTQSPAIMSASPGKVTITCSASSSYNMHWFOQKPGTSPKLIWYSTSNLASGVPAR 79
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 80 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 125

Claim 63; Page 62-63; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a
XX complex of two polypeptides (P1) and two second polypeptides (P2) which
XX are stably associated in an immunoglobulin like complex. P1 has an
XX antigen-binding site located to the N terminus of immunoglobulin (Ig)
XX light chain constant domain (CL domain), and P2 has an antigen-binding
XX site located to the N terminus of the CH1 domain. (I) is useful for:
XX neutralising the activation of a vascular endothelial growth factor
XX (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
XX reducing endothelial cell proliferation; inhibiting VEGF induced
XX migration of human leukaemia cells; blocking interaction of a protein and
XX its ligand; promoting interactions between immune cells and target cells;
XX and in vivo and in vitro for investigative, diagnostic or treatment
XX methods. The design of (I) provides for efficient production so that
XX substantially all of the antigen-binding proteins produced are assembled
XX in the desired configuration. (I) is bivalent and bispecific, homogeneous
XX and in tetrameric form. The heavy chain constant domains which constitute
XX the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
XX antibody and which provide other antibody functions can be present. There
XX is no requirement for processing in vitro to obtain the complete product.
XX This is the amino acid sequence of a single chain variable fragment
XX (scFv), an engineered protein containing a variable light and variable
XX heavy domain on one polypeptide, described in the method of the
XX invention.

SQ Sequence 238 AA;

Query Match: 100.0%; Score 549; DB 23; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPALMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYTSNLSASGVPAR 60
DB 133 DIELTQSPALMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYTSNLSASGVPAR 192

QY 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

DB 193 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238

RESULT 9

ID AAU74419 standard; Protein; 240 AA.

XX AAU74419;

XX 26-MAR-2002 (first entry)

DE Antigen-binding protein, single chain variable fragment version #1.

XX Antigen-binding protein; single chain variable fragment; scFv; antigen;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.

XX Mus sp.
OS Synthetic.

XX Key Location/Qualifiers

FT Region 1..117

FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"

FT Region 118..132

FT /label= Linker

FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"

FT Region 133..240

FT /label= VL

FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"

XX WO200190192-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US16924.

XX 24-MAY-2000; 2000US-206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z;

XX WPI; 2002-106189/14.

XX New bispecific immunoglobulin-like antigen-binding protein for reducing
XX tumour growth and for inhibiting angiogenesis, comprises a complex of
XX two polypeptides and two second polypeptides

XX Claim 63; Page 62; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a
XX complex of two polypeptides (P1) and two second polypeptides (P2) which
XX are stably associated in an immunoglobulin like complex. P1 has an
XX antigen-binding site located to the N terminus of immunoglobulin (Ig)
XX light chain constant domain (CL domain), and P2 has an antigen-binding
XX site located to the N terminus of the CH1 domain. (I) is useful for:
XX neutralising the activation of a vascular endothelial growth factor
XX (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
XX reducing endothelial cell proliferation; inhibiting VEGF induced
XX migration of human leukaemia cells; blocking interaction of a protein and
XX its ligand; promoting interactions between immune cells and target cells;
XX and in vivo and in vitro for investigative, diagnostic or treatment
XX methods. The design of (I) provides for efficient production so that
XX substantially all of the antigen-binding proteins produced are assembled
XX in the desired configuration. (I) is bivalent and bispecific, homogeneous
XX and in tetrameric form. The heavy chain constant domains which constitute
XX the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
XX antibody and which provide other antibody functions can be present. There
XX is no requirement for processing in vitro to obtain the complete product.
XX This is the amino acid sequence of a single chain variable fragment
XX (scFv), an engineered protein containing a variable light and variable
XX heavy domain on one polypeptide, described in the method of the
XX invention.

SQ Sequence 240 AA;

Query Match: 100.0%; Score 549; DB 23; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPALMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYTSNLSASGVPAR 60
DB 133 DIELTQSPALMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYTSNLSASGVPAR 192

QY 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

DB 193 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 238

RESULT 10

ID AAB70842

XX AAB70842 standard; Protein; 330 AA.

XX AAB70842;

XX 25-JUN-2001 (first entry)

XX SNV-env leader/human 7B2-scFv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;

acquired immune deficiency syndrome; severe combined immune deficiency;
T cell lymphoma; fusion construct.

Chimeric - Homo sapiens.
Chimeric - Spleen necrosis virus.

Key Location/Qualifiers
Protein 1..45
/label= SNV-env_leader
Protein 46..330
/label= 7b2-scfv

DE19946142-A1.

29-MAR-2001.

27-SEP-1999; 99DE-1046142.

27-SEP-1999; 99DE-1046142.

(BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.

Cichutek K, Engelstaedter M;

WPI; 2001-246140/26.

N-PSDB; AAF61511.

Cell-targeting vector selective for T lymphocytes, useful in gene
therapy of e.g. acquired immune deficiency syndrome, encodes a
single-chain variable antibody fragment -

Claim 1; Fig 3; 18pp; German.

This invention describes a novel cell-targeting vector (A) containing a
DNA sequence (I) encoding a single-chain variable antibody fragment
(scfv). The products of the invention have antiviral, cytostatic and
immunostimulant activity and can be used in gene therapy, immunization
and diagnosis particularly of T cell-associated diseases, specifically
acquired immune deficiency syndrome (AIDS), severe combined immune
deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
human B cells, and 1000 fold selectivity over other human cells. A vector
designated 7A5 encodes a 329 amino acid single-chain variable antibody
fragment, fully defined in the specification. It was used to transform
D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
(SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
carcinoma) cells. After 48 hours, the cells were stained with x-gal to
determine transfection. The viral titer (infectious units/ml) was over
1 million for D17, 1 million for C8166 but less than 100 for HeLa,
showing the high selectivity for human T cells. This sequence represents
the SNV-env leader/human 7b2-scfv fusion construct used in the
construction of novel cell targeting vectors described in the invention.

Sequence 330 AA;

Query Match 100.0%; Score 549; DB 22; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.6e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIELTQSPAINSPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTSNLASHGVPAR 60
|||||
Db 181 DIELTQSPAINSPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTSNLASHGVPAR 240
|||||

Qy 61 FSGSGSGTYSLTISRMEADAAATYYCQORSSYPPTFGSGTKLEIK 106
|||||
Db 241 FSGSGSGTYSLTISRMEADAAATYYCQORSSYPPTFGSGTKLEIK 286
|||||

RESULT 11

AAR79884

ID AAR79884 standard; Protein; 108 AA.

XX

AC AAR79884;

02-JUL-1996 (first entry)

Anti-EGFR antibody light chain variable region (Clone L2 8C).

Single chain antibody; antibody; epidermal growth factor receptor;
EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
assessment; phage antibody library.

Mus musculus.

Key Location/Qualifiers

Region 1..23

/label= Framework region 1.

Region 24..33

/label= CDR1.

Region 34..48

/label= Framework region 2.

Region 49..55

/label= CDR2.

Region 56..87

/label= Framework region 3.

Region 88..96

/label= CDR3.

Region 97..108

/label= Framework region 4.

WO9525167-A1.

21-SEP-1995.

16-MAR-1995; 95WO-EP00978.

02-DEC-1994; 94EP-0118970.

17-MAR-1994; 94EP-0104160.

(MERE) MERCK PATENT GMBH.

Adan J, Ansell KH, Bendig MM, Blasco F, Gnessow D;
Kettleborough AC, Mitjans F, Plauts J, Rosell E;

WPI; 1995-336972/43.

Anti-EGFR antibodies and single chain Fv antibody fragments -
obtained from phage-antibody libraries, useful for diagnosis and
therapy of tumours

Disclosure; Figure 1A; 93pp; English.

Anti-epidermal growth factor receptor (EGFR) single chain antibodies
and antibodies constructed from anti-EGFR antibody fragments can be
used for diagnosis of tumours and assessment of tumour growth in
vitro and in vivo. They may also be used in a pharmaceutical
composition for the therapy of e.g. melanomas, gliomas and carcinomas.
The antibodies and fragments are derived from mice but are humanised
so as to cause minimum reaction against them. They are produced
using the phage antibody library.

Sequence 108 AA;

Query Match 97.3%; Score 534; DB 16; Length 108;
Best Local Similarity 96.2%; Pred. No. 6.6e-31;
Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIELTQSPAINSPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTSNLASHGVPAR 60
|||||
Db 1 DIELTQSPAINSPGKVTITCSASSVSVMHWFQKPGTSPKLIWYSTSNLASHGVPAR 60
|||||

Qy 61 FSGSGSGTYSLTISRMEADAAATYYCQORSSYPPTFGSGTKLEIK 106
|||||

Db 61 FSGSGSGTYSLTISRMEADAAATYYCQORSSYPPTFGAGTKLEIK 106
|||||

RESULT 12
AAW41392 ID: AAW41392 standard; Protein; 235 AA.
XX AC AAW41392;
XX DT 02-JUN-1998 (first entry)
XX DE Chimeric anti-CEA antibody 806.077 light chain.
KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region; light chain.
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Mus sp.
XX PN W09742329-A1.
XX PD 13-NOV-1997.
XX PF 29-APR-1997; 97WO-GB01165.
XX PR 14-FEB-1997; 97GB-0003103.
XX PR 04-MAY-1996; 96GB-0009405.
XX PA (ZENE) ZENECA LTD.
XX PI Copley CG, Edge MD, Emery SC;
XX WPI; 1997-558987/51.
XX DR N-PSDB; AAV17288.
XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
XX diagnosis and therapy of cancer
XX Example 6; Page 100-101; 208pp; English.
XX This sequence is the light chain variable region of the antibody of
the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
antibody (806.077 Ab). Host cells or transgenic organisms transformed
with DNA encoding the antibody, are used to make the antibody or
conjugate. The conjugate is used in a medicament suitable for intravenous
administration. The conjugate can be used for cancer therapy, selectively
killing tumour cells. The antibody can be used for in vivo or in vitro
diagnosis of cancer.
XX Sequence 235 AA;
Query Match 97.3%; Score 534; DB 18; Length 235;
Best Local Similarity 96.2%; Pred. No. 1.3e-30;
Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSAPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSAGVPPAR 60
DB 23 DIELTQSPAIMSAPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSAGVPPAR 82
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106
DB 83 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 128
RESULT 13
AAR21290 ID: AAR21290 standard; Protein; 108 AA.
XX AC AAR21290;
XX DT 21-MAY-1992 (first entry)
XX DE Murine VL kappa group VI chain "e", specific for phox.
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW

KW specific binding pairs; replicable genetic display package.
XX Synthetic.
XX Key Location/Qualifiers
FH Binding-site 24..33
FT /label= CDR1
FT Binding-site 49..55
FT /label= CDR2
FT Binding-site 88..96
FT /label= CDR3
FT /note=" D-X-G-X-X motif "
XX W09201047-A.
XX 23-JAN-1992.
XX PF 10-JUL-1991; 91WO-GB01134.
XX PR 15-MAY-1991; 91GB-0010549.
XX PR 10-JUL-1990; 90GB-0015198.
XX PR 19-OCT-1990; 90GB-0022845.
XX PR 12-NOV-1990; 90GB-0024503.
XX PR 06-MAR-1991; 91GB-0004744.
XX (CAMP-) CAMBRIDGE ANTIBODY.
XX (MEDI-) MED RES COUNCIL.
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
XX Winter GP, Bonnett TP;
XX WPI; 1992-056862/07.
XX Producing members of specific binding pairs - by expression in
recombinant host cells with a secreting replicable genetic
display package.
XX Example 21; Fig 24; 209pp; English.
XX The VK sequence is one of seven (AAR21286-92) found to be expressed
from a single chain Fv library from an immunised mouse. The libra-
ry produces a diverse repertoire of antibody fragments specific for
2-phenyl-5-oxazolone (phOx). It was prep'd. using cDNA generated
from mRNA from mice immunised with phOx coupled to chicked serum
albumin. The VH and VL kappa sequences were separately amplified
by PCR (see AAR23474-84) and ligated into fcaR2 (see AAR23463) for ex-
pression on the phage surface as fusions with gene III. The result-
ing library of clones was diverse. Twenty three hapten binding
clones were sequenced revealing eight different VH genes (A-H) (see
AAR21264-71) in a variety of pairings with the seven different Vk
genes (a-g). Of the twenty three clones sequenced, four were of
type "e", and were "ox-like" genes. (See Berec et al, Nature 316
412-418, 1985). They contain the DXGXX motif in CDR3, the central
gly of which is needed to create a cavity for phox. Most of the
clones were VK-d combinations. The Kd of VH-B/Vk-b for phox-CABA
was 10 uM, one of the highest values found. This suggests that
phage bearing scfv fragments having weak affinities can be selected
with antigen, probably due to the avidity of the multiple antibody
heads on the phage.
XX See also AAR21260-307, 309-311; AAR22450, 565-581.
XX Sequence 108 AA;
Query Match 96.9%; Score 532; DB 13; Length 108;
Best Local Similarity 97.2%; Pred. No. 9.2e-31;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSAPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSAGVPPAR 60
DB 1 DIELTQSPAIMSAPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSAGVPPAR 60
QY 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

Db 61 FSGSGGTSYSLTISRMEADAATYCCQORSSYPPTFGSGTKLEIK 106
|||||

RESULT 14

AAW41388
ID AAW41388 standard; Protein; 108 AA.

XX AC AAW41388;

XX DT 02-JUN-1998 (first entry)

XX DE Anti-CEA antibody 806.077 light chain variable region.

XX KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
cancer diagnosis; complementarity determining region; light chain.

XX OS Synthetic.

XX PN WO9742329-A1.

XX PD 13-NOV-1997.

XX PF 29-APR-1997; 97WO-GB01165.

XX PR 14-FEB-1997; 97GB-0003103.

XX PR 04-MAY-1996; 96GB-0009405.

XX PA (ZENE) ZENECA LTD.

XX PI Copley CG, Edge MD, Emery SC;

XX DR WPI; 1997-558987/51.

XX DR N-PSDB; AAV17270.

XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
diagnosis and therapy of cancer

XX PS Claim 3; Page 196; 208pp; English.

XX CC This sequence is the light chain variable region of the antibody of
the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
antibody (806.077 Ab). Host cells or transgenic organisms transformed
with DNA encoding the antibody, are used to make the antibody or
conjugate. The conjugate is used in a medicament suitable for intravenous
administration. The conjugate can be used for cancer therapy, selectively
killing tumour cells. The antibody can be used for in vivo or in vitro
diagnosis of cancer.

XX SQ Sequence 108 AA;

Query Match 96.9%; Score 532; DB 18; Length 108;
Best Local Similarity 95.3%; Pred. No. 9.2e-31;
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMASPGKVKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPAR 60
|||||

Db 1 DIELTQSPAIMASPGKVKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPAR 60
|||||

Qy 61 FSGSGGTSYSLTISRMEADAATYCCQORSSYPPTFGSGTKLEIK 106
|||||

Db 61 FSGSGGTSYSLTISRMEADAATYCCQORSTYPLTFGAGTKLEIK 106
|||||

RESULT 15

AAB83159
ID AAB83159 standard; protein; 107 AA.

XX AC AAB83159;

XX DT 02-JUL-2001 (first entry)

XX DE Mouse ganglioside GM2 antibody-related protein #2.

XX KW Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX OS Mus sp.

XX PN WO200123431-A1.

XX PD 05-APR-2001.

XX PF 29-SEP-2000; 2000WO-JP06775.

XX PR 30-SEP-1999; 99JP-0278292.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Hanai N, Nakamura K, Niwa R;

XX DR WPI; 2001-266142/27.

XX PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
radioisotopes or proteins for treatment and diagnosis of cancer -

XX PS Claim 29; Page 69-70; 80pp; Japanese.

XX CC The present invention relates to derivatives of an antibody against
ganglioside GM2. The antibody may be a monoclonal antibody or its
fragments. The antibody is combined with a radioactive isotope,
protein or small drug in the treatment and diagnosis of cancer.

XX SQ Sequence 107 AA;

Query Match 96.4%; Score 529; DB 22; Length 107;

Best Local Similarity 97.1%; Pred. No. 1.5e-30;

Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMASPGKVKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARF 61
|||||

Db 2 IELTQSPAIMASPGKVKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTNLSASGVPARF 61
|||||

Qy 62 SGSGSGTSYSLTISRMEADAATYCCQORSSYPPTFGSGTKLEIK 106
|||||

Db 62 SGSGSGTSYSLTISRMEADAATYCCQORSSYPPTFGSGTKLEIK 106
|||||

Search completed: December 23, 2002, 07:25:10

Job time : 56.9031 secs

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; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-21

Query Match 100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | |
Db 1 WIDPENGSDYAPKFG 17

RESULT 3

US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | |
Db 50 WIDPENGSDYAPKFG 66

RESULT 4

US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match 100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | |
Db 50 WIDPENGSDYAPKFG 66

RESULT 5

US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

Query Match 100.0%; Score 101; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | |
Db 50 WIDPENGSDYAPKFG 66

RESULT 6

US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match 100.0%; Score 101; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | |
Db 50 WIDPENGSDYAPKFG 66

RESULT 7

US-09-976-787-2

; Sequence 2, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-2

Query Match 93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 WIDPENGSGYAPKFG 17

RESULT 8

US-09-865-198-2
; Sequence 2, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2

Query Match 93.1%; Score 94; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 WIDPENGSGYAPKFG 17

RESULT 9

US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7

Query Match 93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 9.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 WIDPENGSGYAPKFG 66

RESULT 10

US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

Query Match 93.1%; Score 94; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 9.7e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFG 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 WIDPENGSGYAPKFG 66

RESULT 11

US-09-974-052-1
; Sequence 1, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124


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US-09-974-052-6
; Sequence 6, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 6
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHAA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMV VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27,
; OTHER INFORMATION: Ile-29, Lys-30, Ala-97, and Thr-98
; US-09-974-052-6

```

Query Match 93.1%; Score 94; DB 9; Length 124;
Best Local Similarity 88.2%; Pred. No. 1e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDYAPKFQ 17
 |||||:|||||
 Db 50 WIDPENGDTYAPKFQ 66

Search completed: December 23, 2002, 07:58:20
Job time : 1.5814 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 57.9767 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-8

Perfect score: 538

Sequence: 1 DIETQSPALMSASPGKVT.....QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	100.0	108	21	AA197236
2	558	100.0	108	22	AA197236
3	558	100.0	108	23	AA197236
4	558	100.0	240	23	AAU74413
5	558	100.0	330	22	AAU74419
6	549	98.4	106	22	AA19842
7	549	98.4	106	22	AA19842
8	549	98.4	125	22	AA19842
9	549	98.4	125	22	AA19842
10	549	98.4	238	22	AAU74420

11	543	97.3	108	16	AA197984
12	541	97.0	108	13	AA197984
13	541	97.0	108	18	AA197984
14	539	96.6	235	18	AA197984
15	536	96.1	256	22	AA197984
16	536	96.1	258	22	AA197984
17	534	95.7	107	22	AA197984
18	534	95.7	129	15	AA197984
19	534	95.7	129	20	AA197984
20	534	95.7	129	20	AA197984
21	533	95.5	108	13	AA197984
22	532	95.3	270	16	AA197984
23	532	95.3	553	18	AA197984
24	532	95.3	553	20	AA197984
25	532	95.3	553	22	AA197984
26	532	95.3	553	22	AA197984
27	531	95.2	107	22	AA197984
28	528	94.6	236	20	AA197984
29	526	94.3	281	20	AA197984
30	526	94.3	666	20	AA197984
31	524	93.9	109	23	AA197984
32	519	93.0	556	22	AA197984
33	519	93.0	556	22	AA197984
34	518	92.8	105	17	AA197984
35	516	92.5	106	13	AA197984
36	516	92.5	106	19	AA197984
37	516	92.5	106	22	AA197984
38	516	92.5	106	22	AA197984
39	516	92.5	128	10	AA197984
40	516	92.5	239	21	AA197984
41	516	92.5	239	22	AA197984
42	516	92.5	599	19	AA197984
43	516	92.5	599	20	AA197984
44	516	92.5	599	21	AA197984
45	511	91.6	128	21	AA197984

ALIGNMENTS

RESULT 1

AA197236

ID AA197236 standard; Protein: 108 AA.

AC AA197236;

DT 19-DEC-2000 (first entry)

XX Variable light chain fragment of anti-SI(KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR;

KW VEGF; vascular endothelial growth factor; KDR;

KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diabody; triabody;

KW glioblastoma multiforme; hemangioblastoma; AIDS;

KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;

KW acquired immune deficiency syndrome; AIDS; human.

XX Homo sapiens.

OS Synthetic.

XX WO200044777-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US02180.

XX 29-JAN-1999; 99US-0117726.

XX 29-JAN-1999; 99US-0240736.

XX (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z, Witte L;

Anti-EGFR antibody
Murine VL kappa gr
Anti-CEA antibody
Chimeric anti-CEA
Anti-p53 common mu
Anti-p53 common mu
Mouse ganglioside
KM-796 and KM-750
Anti-GM2 light cha
Antibody chain use
Murine VL kappa gr
MFE-23 antibody.
Single chain anti-
H22-anti-CEA antib
Bispecific single
Bispecific single
Amino acid sequenc
Partial amino acid
Fusion protein PIC
Fusion protein (80
Murine trkC antibo
scFv-rearranged ca
scFv-rearranged ca
Guy's 13 anti-Stre
Anti-Tac light cha
Protein SEQ ID NO:
Murine anti-Tac an
Murine anti-Tac an
Protein encoded by
Anti-Tac sfv prote
Anti-Tac sfv prote
Anti-Tac(Fv)-PE40
Anti-Tac(Fv)-PE40
Anti-Tac(Fv)-PE40
Mouse monoclonal a

```

XX WPI: 2000-505966/45.
DR N-PSDB: AAA53768.
XX
XX Novel immunoglobulin molecules binding kinase insert domain-containing
XX receptor with the same affinity as vascular endothelial growth factor,
XX used to reduce tumour growth
XX
XX Claim 4; Page 51; 55pp; English.
XX
XX New immunoglobulin molecules are described that bind kinase insert
XX domain-containing receptor (KDR) with a comparable affinity to human
XX vascular endothelial growth factor (VEGF). The antibodies neutralise
XX KDR activation. The immunoglobulin may be a multivalent single
XX chain antibody, a monovalent single chain antibody, a diabody, a
XX triabody, a humanised antibody or a chimerised antibody.
XX The immunoglobulin molecules bind specifically to an
XX extracellular domain of the KDR receptor with the same affinity as
XX VEGF. Overexpression of VEGF has been implicated in a number of
XX human tumour cell lines including glioblastoma multiforme,
XX hemangioblastoma, central nervous system neoplasms and AIDS
XX associated Kaposi's sarcoma. The antibodies therefore have
XX applications in treating these conditions. This sequence encodes a
XX preferred heavy chain complementary determining region of the
XX immunoglobulins of the invention.
XX
XX Sequence: 108 AA;
XX
XX Query Match: 100.0%; Score 558; DB 21; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-32;
XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DIETQSPALMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVGP 60
XX DB 1 DIETQSPALMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVGP 60
XX
XX QY 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
XX DB 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
XX
XX RESULT 2
XX AAB82710 standard; Protein; 108 AA.
XX
XX AC AAB82710;
XX
XX DT 15-OCT-2001 (first entry)
XX
XX VEGF antagonist antibody IMC-1C11 light chain variable region.
XX
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
XX vascular endothelial growth factor; angiogenesis; antiangiogenic;
XX antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
XX tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
XX colon carcinoma; ovarian carcinoma; neuroblastoma;
XX glioblastoma multiforme; melanoma; therapy; light chain.
XX
XX Chimeric - Mus sp.
XX Chimeric - Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Region 24..33
XX FT /label= CDR-L1
XX FT /note= "complementarity determining region 1"
XX FT Region 49..55
XX FT /label= CDR-L2
XX FT /note= "complementarity determining region 2"
XX FT Region 88..96
XX FT /label= CDR-L3
XX FT /note= "complementarity determining region 3"
XX
XX WO200154723-A1.

```

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XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US02839.
XX
XX 28-JAN-2000; 2000US-0178791.
XX 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Kerbel R;
XX
XX WPI: 2001-514531/56.
XX N-PSDB: AAH26406.
XX
XX Treating or controlling an angiogenic dependent condition (e.g. a
XX neoplasm, collagen-vascular or autoimmune disease) in mammal by
XX administering a combination of an antiangiogenic molecule and a
XX chemotherapeutic agent
XX
XX Disclosure; Page 38-39; 42pp; English.
XX
XX The present sequence is that of the light chain variable region of
XX IMC-1C11, a mouse-human chimeric antibody that has vascular
XX endothelial growth factor (VEGF) antagonist activity. The antibody,
XX or a fragment of it, can be used as an anti-angiogenic molecule,
XX together with a chemotherapeutic acid, for the treatment of an
XX angiogenic dependent condition in a mammal, especially a human.
XX The invention relates generally to a method of treating or
XX controlling an angiogenic dependent condition by administering an
XX anti-angiogenic molecule and a chemotherapeutic agent, to produce a
XX regression or arrest of the condition while minimising or
XX preventing significant toxicity of the chemotherapeutic agent.
XX The anti-angiogenic molecule inhibits or blocks the action of a
XX vascular endothelium survival factor such as VEGF or its receptor,
XX and is especially IMC-1C11. Conditions that can be treated include
XX a neoplasm, a collagen-vascular disease or an autoimmune disease,
XX especially a solid tumour; including breast carcinoma, lung
XX carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
XX ovarian carcinoma, neuroblastoma, central nervous system tumour,
XX neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
XX
XX Sequence 108 AA;
XX
XX Query Match: 100.0%; Score 558; DB 22; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-32;
XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DIETQSPALMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVGP 60
XX DB 1 DIETQSPALMSASPGKVTITCSASSSVSYMHWFQKPGTSPKLIWYSTNLSAGVGP 60
XX
XX QY 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
XX DB 61 FSGSGSGTSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKRA 108
XX
XX RESULT 3
XX AAU74413 standard; peptide; 108 AA.
XX
XX AC AAU74413;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Antigen-binding protein light chain variable domain (VH) #1.
XX
XX Antigen-binding protein; antibody light chain variable domain;
XX cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
XX vascular endothelial growth factor receptor; VEGF;
XX cell proliferation inhibitor.
XX

```


Db 133 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 192
QY 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 108
Db 193 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 240

RESULT 5
AAB70842
ID AAB70842 standard; Protein; 330 AA.
XX AAB70842;
DT 25-JUN-2001 (first entry)
XX SNV-env leader/human 7B2-scfv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.

XX Chimeric - Homo sapiens.
OS Chimeric - Spleen necrosis virus.
XX Key Location/Qualifiers
FH 1..45
FT Protein /label= SNV-env_leader
FT 46..330
FT Protein /label= 7B2-scfv

XX DE19946142-A1.
XX 29-MAR-2001.
XX 27-SEP-1999; 99DE-1046142.
XX 27-SEP-1999; 99DE-1046142.
XX (BUND)BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
XX Cichutek K, Engelstaedter M;
XX WPI; 2001-246140/26.
XX N-PSDB; AAF61511.

XX Cell-targeting vector selective for T lymphocytes, useful in gene
PT therapy of e.g. acquired immune deficiency syndrome, encodes a
PT single-chain variable antibody fragment -
XX Claim 1; Fig 3; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scfv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human/B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transfection. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 7B2-scfv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.

XX SQ Sequence 330 AA;
Query Match 100.0%; Score 558; DB 22; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 60
Db 181 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTNLSASGVPAR 240
QY 61 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 108
Db 241 FSGSGSGTSYSLTISRMEADAATYYCOORSSYPPTFGSGTKLEIKRA 288

RESULT 6
AAE13144
ID AAE13144 standard; Protein; 106 AA.
XX AAE13144;
XX 28-JAN-2002 (first entry)
XX Humanised antibody light chain fragment.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.

XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX WO200174296-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10504.
XX 31-MAR-2000; 2000US-0540770.
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (CORR) CORNELL RES FOUND INC.
XX Witte L, Rafii S;
XX WPI; 2001-662942/76.
XX N-PSDB; AAD21670.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX Claim 8; Page 16; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody light chain fragment used in the exemplification of the
CC invention.

XX SQ Sequence 106 AA;

Query Match 98.4%; Score 549; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTSQPAIMASPGCEKVTITCSASSSVSYMHWFQQKPGTSPKLIWYSTNLSAGVGP 60
|||||
Db 1 DIELTSQPAIMASPGCEKVTITCSASSSVSYMHWFQQKPGTSPKLIWYSTNLSAGVGP 60
|||||

QY 61 FSGSGGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
|||||
Db 61 FSGSGGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIK 106
|||||

RESULT 7
AAU74418
ID AAU74418 standard; peptide; 106 AA.
XX AC AAU74418;
XX DT 26-MAR-2002 (first entry)
XX DE Antigen-binding protein light chain variable domain (VH) #2.
XX KW Antigen-binding protein; antibody light chain variable domain;
KW cytotactic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX OS Mus sp.
XX PN WO200190192-A2.
XX PD 29-NOV-2001.
XX PF 24-MAY-2001; 2001WO-US16924.
XX PR 24-MAY-2000; 2000US-206749P.
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z;
XX WPI; 2002-106189/14.
XX N-PSDB; AAU20289.

New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides -

Claim 61; Page 61; 64pp; English.

The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an Ig molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in

CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric
CC p1c11 light chain fragment which is used for the construction of chimeric
CC p1c11 IgG expression vector. Chimeric p1c11 light chain contains cloned
CC variable light chain (VL) and human kappa light chain constant region
CC (CL).

XX Sequence 125 AA;

Query Match 98.4%; Score 549; DB 22; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.2e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTITCSASSVSYMHWFQKPGTSPKLIWYSTNLSAGVDPAR 60

Db 20 DIETQSPAIMSASPGKVTITCSASSVSYMHWFQKPGTSPKLIWYSTNLSAGVDPAR 79

Qy 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

Db 80 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 9

AAAB82702

ID AAB82702, standard; Protein; 125 AA.

XX

AC AAB82702;

XX

DT 15-OCT-2001 (first entry)

XX

DE VEGF antagonist antibody IMC-1C11 light chain variable region.

XX

KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;

KW vascular; endothelial growth factor; angiogenesis; antiangiogenic;

KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;

KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;

KW colon carcinoma; ovarian carcinoma; neuroblastoma;

KW glioblastoma multiforme; melanoma; therapy; light chain.

XX

OS Chimeric - Mus sp.

OS

XX Chimeric - Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Signal_peptide

FT Protein 20..125

FT /label= Mature_protein

FT Region 43..52

FT /label= CDR-L1

FT /note= "complementarity determining region 1"

FT Region 68..74

FT /label= CDR-L2

FT /note= "complementarity determining region 2"

FT Region 107..115

FT /label= CDR-L3

FT /note= "complementarity determining region 3"

XX

PN WO200154723-A1.

XX

PD 02-AUG-2001.

XX

PF 29-JAN-2001; 2001WO-US02839.

XX

PR 28-JAN-2000; 2000US-0178791.

XX

PR 31-MAR-2000; 2000US-0539692.

XX

PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.

PA (IMCL-) IMCLONE SYSTEMS INC.

XX

PI Kerbel R;

XX

XX WPI; 2001-514531/56.

DR

DR N-PSDB; AAH26414.

XX

XX Treating or controlling an angiogenic dependent condition (e.g. a
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
PT administering a combination of an antiangiogenic molecule and a
PT chemotherapeutic agent

XX

PS Disclosure; Fig 1; 42pp; English.

XX

XX The present sequence is that of the light chain variable region of
CC IMC-1C11, a mouse-human chimeric antibody that has vascular
CC endothelial growth factor (VEGF) antagonist activity. The antibody,
CC or a fragment of it, can be used as an anti-angiogenic molecule,
CC together with a chemotherapeutic acid, for the treatment of an
CC angiogenic dependent condition in a mammal, especially a human.

CC The invention relates generally to a method of treating or
CC controlling an angiogenic dependent condition by administering an
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
CC regression or arrest of the condition while minimising or
CC preventing significant toxicity of the chemotherapeutic agent.

CC The anti-angiogenic molecule inhibits or blocks the action of a
CC vascular endothelium survival factor such as VEGF or its receptor,
CC and is especially IMC-1C11. Conditions that can be treated include
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC especially a solid tumour, including breast carcinoma, lung
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX Sequence 125 AA;

Query Match 98.4%; Score 549; DB 22; Length 125;

Best Local Similarity 100.0%; Pred. No. 9.2e-32;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTITCSASSVSYMHWFQKPGTSPKLIWYSTNLSAGVDPAR 60

Db 20 DIETQSPAIMSASPGKVTITCSASSVSYMHWFQKPGTSPKLIWYSTNLSAGVDPAR 79

Qy 61 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

Db 80 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 10

AAU74420

ID AAU74420 standard; Protein; 238 AA.

XX

XX AAU74420;

XX

DT 26-MAR-2002 (first entry)

XX

DE Antigen-binding protein, single chain variable fragment version #2.

XX

XX Antigen-binding protein; single chain variable fragment; svFv; antigen;
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.

XX

OS Mus sp.

OS

OS Synthetic.

XX

FH Key Location/Qualifiers

XX

FT Region 1..117

FT /label= VH

FT /note= "Heavy chain variable domain. Specifically

FT claimed in claim 61"

FT Region 118..132

FT FT /label= Linker
FT FT /note= "15 amino acid linker joins the VH and VL
FT FT regions of the single chain variable fragment
FT FT protein. Encoded by AAS20285"
FT FT 133..238
FT FT /label= VL
FT FT /note= "Light chain variable domain. Specifically
FT FT claimed in claim 61"
XX WO200190192-A2.
XX 29-NOV-2001.
PD XX
XX 24-MAY-2001; 2001WO-US16924.
XX 24-MAY-2000; 2000US-206749P.
XX (IMCL-) IMCLONE SYSTEMS INC.
PA Zhu Z;
PI WPI; 2002-106189/14.
DR New bispecific immunoglobulin-like antigen-binding protein for reducing
XX tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
PT two polypeptides and two second polypeptides
XX Claim 63; Page 62-63; 64pp; English.
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (scFv), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
XX invention.
SQ Sequence 238 AA;
Query Match 98.4%; Score 549; DB 23; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.6e-31;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQKPCTSPKLIYTSNLSGVAP 60
Db 133 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQKPCTSPKLIYTSNLSGVAP 192
QY 61 FSGSGSGTSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 106
Db 193 FSGSGSGTSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 238
RESULT 11
AAR79884
ID AAR79884 standard; Protein; 108 AA.
XX
AC AAR79884;

XX 02-JUL-1996 (first entry)
DT Anti-EGFR antibody light chain variable region (Clone L2 8C).
DE Single chain antibody; antibody; epidermal growth factor receptor;
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
KW assessment; phage antibody library.
XX Mus musculus.
XX Key Location/Qualifiers
FH Region 1..23 /label= Framework region 1.
FT Region 24..33 /label= CDR1.
FT Region 34..48 /label= Framework region 2.
FT Region 49..55 /label= CDR2.
FT Region 56..87 /label= Framework region 3.
FT Region 88..96 /label= CDR3.
FT Region 97..108 /label= Framework region 4.
FT
XX WO9525167-A1.
XX 21-SEP-1995.
XX 16-MAR-1995; 95WO-EP00978.
XX 02-DEC-1994; 94EP-0118970.
PR 17-MAR-1994; 94EP-0104160.
XX (MERE) MERCK PATENT GMBH.
XX Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;
PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;
XX WPI; 1995-336972/43.
XX Anti-EGFR antibodies and single chain Fv antibody fragments -
PT obtained from phage-antibody libraries, useful for diagnosis and
PT therapy of tumours
XX Disclosure; Figure 1A; 93pp; English.
XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC and antibodies constructed from anti-EGFR antibody fragments can be
CC used for diagnosis of tumours and assessment of tumour growth in
CC vitro and in vivo. They may also be used in a pharmaceutical
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC The antibodies and fragments are derived from mice but are humanised
CC so as to cause minimum reaction against them. They are produced
CC using the phage antibody library.
SQ Sequence 108 AA;
Query Match 97.3%; Score 543; DB 16; Length 108;
Best Local Similarity 96.3%; Pred. No. 2.1e-31;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQKPCTSPKLIYTSNLSGVAP 60
Db 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQKPCTSPKLIYTSNLSGVAP 60
QY 61 FSGSGSGTSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIKRA 108
Db 61 FSGSGSGTSLTISRMEADAATYYCQRRSSYPFTFGAGTKLEIKRA 108

RESULT 12

AAAR21290
 ID AAR21290 standard; Protein; 108 AA.
 XX AAR21290;
 AC AAR21290;
 DT 21-MAY-1992 (first entry)
 XX Murine VL kappa group VI chain "e", specific for phox.
 DE
 XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
 KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package.
 XX
 XX Synthetic
 XX
 FH Key Location/Qualifiers
 FT Binding-site 24..33
 FT /label= CDR1
 FT Binding-site 49..55
 FT /label= CDR2
 FT Binding-site 88..96
 FT /label= CDR3
 FT /note=" D-X-G-X-X motif "
 FT
 XX W09201047-A.
 PN
 XX 23-JAN-1992.
 PD
 XX
 PF 10-JUL-1991; 91WO-GB01134.
 XX
 PR 15-MAY-1991; 91GB-0010549.
 PR 10-JUL-1990; 90GB-0015198.
 PR 19-OCT-1990; 90GB-0022845.
 PR 12-NOV-1990; 90GB-0024503.
 PR 06-MAR-1991; 91GB-0004744.
 XX
 PA (CAMB-) CAMBRIDGE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.
 XX
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger RP, Marks JD, Clackson TP, Chiswell DJ;
 PI Winter JGP, Bonnett TP;
 XX
 DR WPI; 1992-056862/07.
 XX
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 PT
 XX Example 21; Fig 24; 209pp; English.
 PS
 XX The V_H sequence is one of seven (AAR21286-92) found to be expressed
 CC from a single chain Fv library from an immunised mouse. The libra-
 CC ry produces a diverse repertoire of antibody fragments specific for
 CC 2-phenyl-5-oxazolone (phox). It was prepd. using cDNA generated
 CC from mRNA from mice immunised with phox coupled to chicked serum
 CC albumin. The V_H and V_L kappa sequences were separately amplified
 CC by PCR (see AAQ23474-84) and ligated into fdCAT2 (see AAQ23463) for ex-
 CC pression on the phage surface as fusions with gene III. The result-
 CC ing library of clones was diverse. Twenty three hapten binding
 CC clones were sequenced revealing eight different V_H genes (A-H) (see
 CC AAR21264-71) in a variety of pairings with the seven different V_L
 CC genes (a-g). Of the twenty three clones sequenced, four were of
 CC type "a-g" and were "ox-like" genes. (See Berak et al, Nature 316
 CC 412-418, 1985). They contain the DXGX motif in CDR3, the central
 CC Gly of which is needed to create a cavity for phox. Most of the
 CC clones were V_k-d combinations. The Kd of V_H-B/V_k-b for phox-GABA
 CC was 50 uM, one of the highest values found. This suggests that
 CC phage bearing scfv fragments having weak affinities can be selected
 CC with antigen, probably due to the avidity of the multiple antibody
 CC heads on the phage.
 CC See also AAR21260-307, 309-311; AAR22450, 565-581.

XX SQ Sequence 108 AA;
 Query Match 97.0%; Score 541; DB 13; Length 108;
 Best Local Similarity 97.2%; Pred. No. 3e-31;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTNLSAGVAPAR 60
 DB 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTNLSAGVAPAR 60
 OY 61 FSGSGSTSYSLTISRMEADAATYYCQRRSSYPPTFGSGTKLEIKRA 108
 DB 61 FSGSGSTSYSLTISRMEADAATYYCQRRSSYPPTFGSGTKLEIKRA 108
 RESULT 13
 AAW41388
 ID AAW41388 standard; Protein; 108 AA.
 XX
 AC AAW41388;
 DT 02-JUN-1998 (first entry)
 XX
 DE Anti-CEA antibody 806.077 light chain variable region.
 XX
 KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
 KW cancer diagnosis; complementarity determining region; light chain.
 XX
 OS Synthetic.
 XX
 PN W09742329-A1.
 XX
 PD 13-NOV-1997.
 XX
 PF 29-APR-1997; 97WO-GB01165.
 XX
 PR 14-FEB-1997; 97GB-0003103.
 PR 04-MAY-1996; 96GB-0009405.
 XX
 PA (ZENÉ) ZENECA LTD.
 XX
 PI Copley CG, Edge MD, Emery SC;
 DR
 DR WPI; 1997-558987/51.
 DR N-PSDB; AAV17270.
 XX
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
 PT diagnosis and therapy of cancer
 XX
 PS Claim 3; Page 196; 208pp; English.
 XX
 CC This sequence is the light chain variable region of the antibody of
 CC the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
 CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
 CC with DNA encoding the antibody, are used to make the antibody or
 CC conjugate. The conjugate is used in a medicament suitable for intravenous
 CC administration. The conjugate can be used for cancer therapy, selectively
 CC killing tumour cells. The antibody can be used for in vivo or in vitro
 CC diagnosis of cancer.
 XX
 SQ Sequence 108 AA;
 Query Match 97.0%; Score 541; DB 18; Length 108;
 Best Local Similarity 95.4%; Pred. No. 3e-31;
 Matches 103; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTNLSAGVAPAR 60
 DB 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQOKPGTSPKLIWYSTNLSAGVAPAR 60
 OY 61 FSGSGSTSYSLTISRMEADAATYYCQRRSSYPPTFGSGTKLEIKRA 108
 DB 61 FSGSGSTSYSLTISRMEADAATYYCQRRSSYPPTFGSGTKLEIKRA 108

Db 61 FSGSGGTSYSLTISRMEADAATYYCQQRSTYPLTFGAGTKLELRA 108

RESULT 14

AAW41392

ID AAW41392 standard; Protein; 235 AA.

XX AC AAW41392;

XX 02-JUN-1998 (first entry)

XX Chimeric anti-CEA antibody 806.077 light chain.

XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region; light chain.
XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.

PN WO9742329-A1.

XX 13-NOV-1997.

XX 29-APR-1997; 97WO-GB01165.

XX 14-FEB-1997; 97GB-0003103.

PR 04-MAY-1996; 96GB-0009405.

XX (ZENE) ZENECA LTD.

XX Copley CG, Edge MD, Emery SC;

PI WPI; 1997-558987/51.

DR N-PSDB; AAV17288.

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
PT diagnosis and therapy of cancer
XX Example 8; Page 100-101; 208pp; English.
XX This sequence is the light chain variable region of the antibody of
CC the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
CC with DNA encoding the antibody, are used to make the antibody or
CC conjugate. The conjugate is used in a medication suitable for intravenous
CC administration. The conjugate can be used for cancer therapy, selectively
CC killing tumour cells. The antibody can be used for in vivo or in vitro
CC diagnosis of cancer.
XX SQ Sequence 235 AA;

Query Match 96.6%; Score 539; DB 18; Length 235;
Best Local Similarity 96.3%; Pred. No. 8.2e-31;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSAPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPAR 60
|||||

Db 23 DIELTQSPAIMSAPGKVTITCSASSSVYMHWFQKPGTSPKLIWYSTSNLASGVPAR 82
|||||

QY 61 FSGSGGTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIKR 107
|||||

Db 83 FSGSGGTSYSLTISRMEADAATYYCQQRSTYPLTFGAGTKLEIKR 129
|||||

RESULT 15

AA82897

ID AA82897 standard; Protein; 256 AA.

XX AC AA82897;

XX 26-NOV-2001 (first entry)

XX Anti-p53 common mutant antigen single chain antibody ME1.

XX Single chain antibody; ME1; mouse; p53; common mutant epitope;
KW tumour suppressor protein; therapy; cancer.
XX OS Mus musculus.

XX Key Location/Qualifiers

XX Region 1..131

FT /label= Heavy_chain

FT Protein 132..256

FT /label= Light_chain

FT Region 27..35

FT /label= CDR1

FT /note= "heavy chain complementarity determining
FT region 1"

FT Region 50..66

FT /label= CDR2

FT /note= "heavy chain complementarity determining
FT region 2"

FT Region 99..105

FT /label= CDR3

FT /note= "heavy chain complementarity determining
FT region 3"

FT Region 155..164

FT /label= CDR1

FT /note= "light chain complementarity determining
FT region 1"

FT Region 180..186

FT /label= CDR2

FT /note= "light chain complementarity determining
FT region 2"

FT Region 219..227

FT /label= CDR3

FT /note= "light chain complementarity determining
FT region 3"

XX WO200168801-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-IL00225.

XX 16-MAR-2000; 2000US-0526738.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Solomon B, Cohen G, Govorko D;

XX WPI; 2001-590047/66.

XX N-PSDB; AAH26790.

XX Novel single chain antibody molecule specifically recognizing common
PT mutant epitope in mutant p53 but not in wild-type p53, and
PT polynucleotides encoding antibodies, useful for preparing medicament
PT for treating cancer -
XX Claim 16; Fig 2A; 46pp; English.

XX The present sequence is that of a single chain antibody (scFv),

CC designated ME1, which specifically recognises the common mutant
CC epitope (see AAB82900) in mutant p53 protein but not in wild-type
CC p53. To obtain the scFv, mice were immunized with the mutant p53
CC epitope peptide. Gene segments encoding the antibody heavy and
CC light chain variable regions were amplified by PCR from the spleen
CC of a hyperimmunised mouse, and a library of the antibody genes was
CC obtained. When the genes isolated from the antibody gene library
CC were assembled in the scFv DNA, expressed as phage antibodies and
CC subjected to panning, scFv ME1 was isolated, which possessed a
CC significant affinity (0.1 uM) towards mutant p53. ME1 was
CC successfully expressed as a soluble antibody, separate from the
CC phage fusion. ME1, DNA encoding it (see AAH26790-91) and a vector
CC comprising the DNA, are used in claimed methods for treating a
CC patient suffering from a disease related to mutation of the p53

CC gene, especially cancer. scfv ME1 serves as a powerful auxiliary
 CC agent capable of specifically enhancing the specificity and
 CC effectiveness of the two major existing anti-cancer gene therapies.
 CC Expression of the scfv ME1 molecules as an intrabody fused to the
 CC F-box domain responsible for the targeting of the cell proteins to
 CC the degradation cascade may be capable of significantly reducing
 CC the level of mutant p53 in the cell, thereby broadening the range
 CC of possible tumour targets for the original therapy. The
 CC substitution of the original antibody by the scfv ME1 specific to
 CC the mutant form of p53 may restrict the therapeutic effect to cancer
 CC cells only, allowing a systemic application of this therapy. ME1
 CC has high specificity, lacks the FC portion which binds specifically
 CC to the antigen, and has high permeability in the cells, and thus is
 CC a suitable probe for immunodiagnostic clinical detection of mutant
 CC p53 in tissues using conventional immunohistochemistry techniques.

XX
 SQ Sequence 256 AA;

Query Match 96.1%; Score 536; DB 22; Length 256;

Best Local Similarity 95.4%; Pred. No. 1.4e-30;

Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYISTSNLASCVPAR 60

DB 132 DIELTOSPAIMASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYISTSNLASCVPAR 191

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIKRA 108

DB 192 FSGSGSGTSYSLTISRMEADAATYYCQORSSYPFTFGSGTKLEIKRA 239

Search completed: December 23, 2002, 07:25:09

Job time : 58.9767 secs

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 62.8081 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-7

Perfect score: 631

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	117	21	AAV97235
2	631	100.0	117	23	AAU74412
3	631	100.0	240	23	AAU74419
4	624	98.9	117	22	AAE13143
5	624	98.9	117	22	AAE13143
6	624	98.9	117	23	AAU74417
7	624	98.9	136	22	AAE13145
8	624	98.9	238	23	AAU74420
9	612	97.0	136	22	AAE13145
10	554.5	87.9	535	18	AAW28491

11	554.5	87.9	535	18	AAW28492	Human p53 protein
12	550.5	87.2	116	21	AAV70787	Murine anti-p53 mo
13	549.5	87.1	243	19	AAW60769	Single chain antib
14	532.5	84.4	112	20	AAW89173	Anti-p53 monoclonal
15	532.5	84.4	118	18	AAW01586	Lead binding MAB 1
16	513.5	81.4	270	16	AAW75719	MFE-23 antibody.
17	513.5	81.4	556	22	AAU97935	ScFv-rearranged ca
18	513.5	81.4	556	22	AAU80040	Anti-carcinomaembryo
19	507.5	80.4	124	15	AAE60566	Anti-carcinomaembryo
20	507.5	80.4	249	19	AAW60770	Single chain anti-
21	507.5	80.4	553	18	AAW11508	Single chain anti-
22	507.5	80.4	553	20	AAW73223	H22-anti-CEA antib
23	507.5	80.4	553	22	AAW85455	Bispecific single
24	507.5	80.4	553	22	AAE61960	Bispecific single
25	503.5	79.8	116	13	AAE24807	RSV19 VH. Mus mus
26	502.5	79.6	116	14	AAE24804	RSV19 heavy chain
27	502.5	79.6	124	15	AAE60565	Anti-carcinomaembryo
28	499.5	79.2	116	14	AAE42802	RSV19 heavy chain
29	499.5	79.2	124	20	AAV39528	Murine COL1 VH cha
30	499.5	79.2	124	23	AAU76632	Murine Col-1(CEA a
31	498.5	79.0	120	18	AAW41387	Anti-CEA antibody
32	498.5	79.0	255	18	AAW41394	Chimeric anti-CEA
33	498.5	79.0	281	20	AAW82744	Fusion protein p1C
34	498.5	79.0	642	20	AAW82741	806.077 heavy chai
35	498.5	79.0	666	20	AAW82745	Fusion protein (80
36	494	78.3	119	12	AAE14394	H3 region of MAB T
37	494	78.3	119	19	AAW48758	TAI antibody VH ch
38	493	78.1	119	12	AAE14395	Modified H3 region
39	487	77.2	140	12	AAE11384	Variable gamma hea
40	486.5	77.1	258	23	ABB05962	Monoclonal antibod
41	486.5	77.1	258	23	ABB05990	Mouse monoclonal a
42	486.5	77.1	258	23	ABB05994	Mouse and human ch
43	486.5	77.1	287	23	ABB05982	Monoclonal antibody
44	484.5	76.8	120	16	AAE79889	Anti-EGFR antibody
45	481.5	76.3	135	21	AAE07967	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAV97235
ID AAV97235 standard; Protein: 117 AA.

XX AC AAV97235;

XX DT 19-DEC-2000 (first entry)

XX DE Variable heavy chain fragment of anti-SI(KDR) antibody.

XX KW Immunoglobulin; antibody; complementary determining region; CDR;

XX KW VEGF; vascular endothelial growth factor; KDR;

XX KW Kinase insert domain containing receptor; multivalent; monovalent;

XX KW Humanised antibody; chimeric antibody; tumour; diabody; triabody;

XX KW glioblastoma multiforme; hemangioblastoma; AIDS;

XX KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;

XX KW acquired immune deficiency syndrome; AIDS; human.

OS Homo sapiens.

OS Synthetic.

XX PN WO200044777-A1.

XX PD 03-AUG-2000.

XX PF 28-JAN-2000; 2000WO-US02180.

XX PR 29-JAN-1999; 99US-0117726.

XX PR 29-JAN-1999; 99US-0240736.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z, Witte L;

XX WPI; 2000-505966/45.
DR N-PSDB; AAS3767.
XX
PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX
PS Claim 4; Page 50-51; 55pp; English.
XX
CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulin of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 631; DB 21; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYHMKVQRPQGLGWIDPENGDSGY 60
DB 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYHMKVQRPQGLGWIDPENGDSGY 60
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGYEGYWGQGTVTYVSS 117
DB 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGYEGYWGQGTVTYVSS 117

RESULT 2
AAU74412
ID AAU74412 standard; peptide; 117 AA.
XX AAU74412;
XX
XX 26-MAR-2002 (first entry)
XX
XX Antigen-binding protein heavy chain variable domain (VH) #1.
XX
XX Antigen-binding protein; antibody heavy chain variable domain;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
XX Mus sp.
XX
XX WO200190192-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US16924.
XX
XX 24-MAY-2000; 2000US-206749P.
XX
XX (INCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2002-106189/14.
DR N-PSDB; AAS20283.
XX

PT New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
PS Claim 57; Page 57; 64pp; English.
XX
CC The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This sequence represents a heavy chain variable domain (VH) incorporated
CC into Fv, an engineered protein containing a heavy chain variable domain
CC and a light chain variable domain in one polypeptide chain, described in
CC the method of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 631; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYHMKVQRPQGLGWIDPENGDSGY 60
DB 1 QVKLQSGAELVGSASVKLSCTTSGFNKDFYHMKVQRPQGLGWIDPENGDSGY 60
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGYEGYWGQGTVTYVSS 117
DB 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYCNAYYGYEGYWGQGTVTYVSS 117

RESULT 3
AAU74419
ID AAU74419 standard; Protein; 240 AA.
XX AAU74419;
XX
XX 26-MAR-2002 (first entry)
XX
XX Antigen-binding protein, single chain variable fragment version #1.
XX
XX Antigen-binding protein; single chain variable fragment; scfv; antigen;
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KW vascular endothelial growth factor receptor; VEGF;
KW cell proliferation inhibitor.
XX
XX Mus sp.
XX Synthetic.
XX
XX Location/Qualifiers
FH 1..117
FT /label= VH
FT /note= "Heavy chain variable domain. Specifically
FT claimed in claim 57"
FT 118..132
FT /label= Linker
FT /note= "15 amino acid linker joins the VH and VL
FT regions of the single chain variable
FT fragment protein. Encoded by AAS20285"

FT Region 133..240
FT /label= VL
FT /note= "Light chain variable domain. Specifically
FT claimed in claim 57"
XX
PN WO200190192-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US1692A.
XX
XX 24-MAY-2000; 2000US-206749P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2002-106189/14.
XX
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumour growth and for inhibiting angiogenesis, comprises a complex of
PT two polypeptides and two second polypeptides
XX
XX Claim 63; Page 62; 64pp; English.
XX
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; inhibiting VEGF induced
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This is the amino acid sequence of a single chain variable fragment
CC (SCFV), an engineered protein containing a variable light and variable
CC heavy domain on one polypeptide, described in the method of the
XX invention.
XX
XX Sequence 240 AA;
XX
XX Query Match 100.0%; Score 631; DB 23; Length 240;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-46;
XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
XX |
XX Db 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
XX |
XX QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVTVSS 117
XX |
XX Db 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVTVSS 117
XX |
XX
XX RESULT 4
XX AAEE13143
XX ID AAEE13143 standard; Protein; 117 AA.
XX AC
XX AAEE13143;
XX
XX 28-JAN-2002 (first entry)
XX
XX Humanised antibody heavy chain fragment.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW human; chimeric.
XX
XX Chimeric - Homo sapiens.
OS
OS Chimeric - Mus sp.
XX
XX WO200174296-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10504.
PF
XX 31-MAR-2000; 2000US-0540770.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX (CORR) CORNELL RES FOUND INC.
PA
XX Witte L, Rafii S;
PI
XX WPI; 2001-662942/76.
XX
XX N-PSDB; AAD21669.
DR
XX
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
PT tumors such as leukemias or multiple myeloma comprises treatment with
PT an antagonist of a vascular endothelial growth factor receptor -
XX
XX Claim 8; Page 15; 68pp; English.
XX
XX The invention relates to a method for inhibiting the growth of non-solid
CC tumour cells that are stimulated by a ligand of vascular endothelial
CC growth factor receptor (VEGFR) in mammals particularly humans. The method
CC involves treating the mammals with humanised VEGFR monoclonal antibodies
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
CC variable region joined to human constant region, where the humanised
CC mouse variable region contains mouse complementarity determining region
CC (CDR) grafted into human variable region. The method is useful for
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
CC multiple myelomas and lymphoid cells, particularly those related to
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
CC antibody heavy chain fragment used in the exemplification of the
XX invention.
XX
XX Sequence 117 AA;
XX
XX Query Match 98.9%; Score 624; DB 22; Length 117;
XX Best Local Similarity 99.1%; Pred. No. 2.8e-46;
XX Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
XX |
XX Db 1 QVKLOQSGAELVGSASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60
XX |
XX QY 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVTVSS 117
XX |
XX Db 61 APKFOGKATMTADSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGQGTITVTVSS 117
XX |
XX
XX RESULT 5
XX AAB82709
XX ID AAB82709 standard; Protein; 117 AA.
XX
XX AAB82709;
XX
XX 15-OCT-2001 (first entry)
XX
XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.
DE
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;

XX DE Human p53 protein variant S-325 encoded by pEC176.
 XX DE
 XX KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.
 XX KW
 XX OS Chimeric - Homo sapiens.
 OS Chimeric - Herpes simplex virus.
 OS Synthetic.
 XX OS
 XX PN WO9704092-A1.
 XX FT
 XX PD 06-FEB-1997.
 XX PF 17-JUL-1996; 96WO-FR01111.
 XX PR 19-JUL-1995; 95FR-0008729.
 XX PA (RHON) RHONE POULENC RORER SA.
 XX PI Bracco L, Conseiller E;
 XX DR N-PSDB; AAT86221.
 XX DR
 XX PT New p53 variants e.g. with oligomerisation domain replaced by
 PT leucine zipper - useful for treating hyper-proliferative disorders,
 PT esp. cancer and restenosis
 XX PT
 XX PS Claim 36; Pages 88-90; 133pp; French.
 XX PS
 XX CC Claimed variants of protein p53 have at least part of the
 CC oligomerisation domain deleted and replaced by a leucine zipper
 CC domain. The mutants preferably also have at least part of the p53
 CC transactivation domain (amino acids 1-74) deleted and replaced by
 CC the transactivating domain (TD) from herpes simplex virus viral
 CC protein VP16 (amino acids 411-490) or by a protein domain able to
 CC bind selectively to a transactivator, especially a single-chain
 CC antibody variable domain (ScFv). The present sequence is that of
 CC a specifically claimed p53 variant designated S-325 and comprising
 CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a
 CC leucine zipper domain at the C-terminal. The p53 variants are
 CC more active and more stable tumour suppressors and apoptosis-inducing
 CC agents than wild-type p53 and are active where the wild-type protein
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic
 CC mutants, nor by other cellular proteins (because the leucine zipper
 CC domain prevents formation of inactive mixed oligomers).
 XX CC
 XX SQ Sequence 535 AA;
 Query Match 87.9%; Score 554.5; DB 18; Length 535;
 Best Local Similarity 88.9%; Pred. No. 1.3e-39;
 Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
 QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEGLEWIGWIDPENGDSGY 60
 Db 3 QVQLQESGAELVSGASVKLSCTASGFNIDYMHVVKORPEGLEWIGWIDPENGDTY 62
 QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDTAVYYCNAYGYEGYWGQGTFTVSS 117
 Db 63 APKFGKATMTADSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGTFTVSS 118
 RESULT 11
 ID AAW28492
 AC AAW28492 standard; Protein: 535 AA.
 AC AAW28492;
 XX AC
 XX DT 25-NOV-1997 (first entry)
 XX DT

DE DE Human p53 protein variant S-325H.
 XX DE
 XX KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.
 XX KW
 XX OS Chimeric - Homo sapiens.
 OS Chimeric - Herpes simplex virus.
 OS Synthetic.
 XX OS
 XX PN WO9704092-A1.
 XX FT
 XX PD 06-FEB-1997.
 XX PF 17-JUL-1996; 96WO-FR01111.
 XX PR 19-JUL-1995; 95FR-0008729.
 XX PA (RHON) RHONE POULENC RORER SA.
 XX PI Bracco L, Conseiller E;
 XX DR WPI; 1997-132633/12.
 XX DR
 XX PT New p53 variants e.g. with oligomerisation domain replaced by
 PT leucine zipper - useful for treating hyper-proliferative disorders,
 PT esp. cancer and restenosis
 XX PT
 XX PS Claim 36; Page -: 133pp; French.
 XX PS
 XX CC Claimed variants of protein p53 have at least part of the
 CC oligomerisation domain deleted and replaced by a leucine zipper
 CC domain. The mutants preferably also have at least part of the p53
 CC transactivation domain (amino acids 1-74) deleted and replaced by
 CC the transactivating domain (TD) from herpes simplex virus viral
 CC protein VP16 (amino acids 411-490) or by a protein domain able to
 CC bind selectively to a transactivator, especially a single-chain
 CC antibody variable domain (ScFv). The present sequence is that of
 CC a specifically claimed p53 variant designated S-325H and comprising
 CC a ScFv domain, amino acids 75-325 of human wild-type p53 (but with
 CC Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
 CC The p53 variants are more active and more stable tumour suppressors
 CC and apoptosis-inducing agents than wild-type p53 and are active where
 CC the wild-type protein is not, i.e. they are not inactivated by dominant
 CC negative or oncogenic mutants, nor by other cellular proteins (because
 CC the leucine zipper domain prevents formation of inactive mixed
 CC oligomers).
 CC (Note: this sequence does not appear in the specification and has
 CC been produced by modifying the given sequence of variant V-325).
 XX CC
 XX SQ Sequence 535 AA;
 Query Match 87.9%; Score 554.5; DB 18; Length 535;
 Best Local Similarity 88.9%; Pred. No. 1.3e-39;
 Matches 104; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
 QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVVKORPEGLEWIGWIDPENGDSGY 60
 Db 3 QVQLQESGAELVSGASVKLSCTASGFNIDYMHVVKORPEGLEWIGWIDPENGDTY 62
 QY 61 APKFGKATMTADSSNTAYLQLSSLTSEDTAVYYCNAYGYEGYWGQGTFTVSS 117
 Db 63 APKFGKATMTADSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGTFTVSS 118
 RESULT 12
 AAY70787


```

XX DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
XX DE Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.
XX OS Mus sp.
XX OS Synthetic.
XX PN W09856416-A1.
XX PD 17-DEC-1998.
XX PF 09-JUN-1998; 98WO-IL00266.
XX PR 09-JUN-1997; 97IL-0121041.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
PI Wolkowicz R;
XX WPI; 1999-070296/06.
XX DR
XX PT Use of a monoclonal antibody to a tumour-associated antigen - to
XX PT induce anti-tumour immunity or elicit an increased immune response
XX PT to the antigen
XX PS Example 3; Fig 3; 47pp; English.
XX CC The present invention describes the use of an immunogen (A) to induce
XX CC anti-tumour immunity; to elicit an increased immune response to tumour
XX CC associated antigen (TAA) and/or to induce an immune response to mutant
XX CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
XX CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
XX CC (complementarity determining region) on the heavy or light chain of MAB
XX CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
XX CC variable (V) region of MAB, in a gene delivery vehicle. The present
XX CC sequence represents the variable heavy chain sequence from anti-p53 MAB
XX CC 421. Also described is a method for generating sequence-specific,
XX CC anti-DNA antibodies (Ab) by immunising a mammal with a MAB directed to a
XX CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
XX CC used to treat a wide variety of primary and metastatic cancers,
XX CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
XX CC to determine critical sequences in animal or plant breeding); to
XX CC identify bacteria and other parasites; to determine parentage; in
XX CC forensic science; to isolate specific genes for DNA vaccination; in gene
XX CC sequencing and cloning; also possibly for activation of selected
XX CC therapeutic genes in plants, animals and humans. (A) induce an effective
XX CC anti-tumour response without causing harm to the patient. The method
XX CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.
XX SQ Sequence 112 AA;
XX Query Match 84.4%; Score 532.5; DB 20; Length 112;
XX Best Local Similarity 88.5%; Pred. No. 1.9e-38;
XX Matches 100; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
XX
XX QY 4 LQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGDSYAPK 63
XX Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
XX 1 LQESGAELVRSGASVKLSCTASGFKDYMKDYMHVWKORPQGLEWIGWIDPENGDEYAPK 60
XX QY 64 FQKATMTADSSNTAYLQLSLTSEDYAVYICNAY-YGDYEGYWGQGTIVTVSS 116
XX Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
XX 61 FQKATMTADTSSNTAYLQLSLASEDTAVYICN-FYGDALDYWGQGTIVTVSS 112
XX
XX RESULT 15
XX AAW01586
XX ID AAW01586 standard; Protein; 118 AA.
XX AC
XX AC AAW01586;
XX XX

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DT 22-AUG-1997 (first entry)
DE Lead binding MAB 14G11 heavy chain variable region.
XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.
XX OS Mus musculus.
XX PN W09639518-A1.
XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US09258.
XX PR 10-OCT-1995; 95US-0541373.
XX PR 05-JUN-1995; 95US-0462798.
XX PA (BION-) BIONEBRASKA INC.
XX PI Lopez O, Murray PJ, Wylie DE;
XX WPI; 1997-043140/04.
XX DR N-PSDB; AAT58260.
XX PT DNA encoding heavy metal binding polypeptide sequences - used for
XX PT detecting, removing, adding or neutralising heavy metals, such as
XX PT lead cations
XX PS Claim 12; Page 75; 125pp; English.
XX CC The present sequence represents the heavy chain variable region for
XX CC monoclonal antibody (MAB) 14G11, which immunoreacts with a lead cation.
XX CC The sequence was derived from RNA isolated from mouse hybridoma cells.
XX CC The protein can be used for binding heavy metals, such as lead cations.
XX CC It can be used for detecting, removing, adding or neutralising the
XX CC heavy metals in biological and inanimate systems. It can be used in
XX CC e.g. aqueous liquid systems, in biological or environmental systems or
XX CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
XX CC care products, skin treatment products, pesticides, herbicides,
XX CC solvents used in the production of semi-conductor and integrated
XX CC circuit components and production materials for electronic components.
XX CC The products can provide for applications involving minute amounts of
XX CC specific heavy metals.
XX SQ Sequence 118 AA;
XX Query Match 84.4%; Score 532.5; DB 18; Length 118;
XX Best Local Similarity 85.6%; Pred. No. 2e-38;
XX Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
XX
XX QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPQGLEWIGWIDPENGDSY 60
XX Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
XX 1 EVQLQSGAELVRSGASVKLSCTASGFKDYMKDYMHVWKORPQGLEWIGWIDPENGDEY 60
XX QY 61 APKFOGKATMTADSSNTAYLQLSLTSEDYAVYICNAY-YGDYEGYWGQGTIVTVSS 117
XX Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
XX 61 DPKFOGKATMTADTSSNTAYLQLSLTSEDYAVYICNPYGYDDAMDYWGQGTIVTVSS 118
XX
XX Search completed: December 23, 2002, 07:25:08
XX Job time : 64.8081 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 1.80233 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-4
Perfect score: 48
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	10	2	US-08-116-778E-9
2	48	100.0	10	2	US-08-438-562-9
3	48	100.0	10	2	US-08-483-528B-97
4	48	100.0	10	3	US-08-836-561-49
5	48	100.0	10	4	US-09-393-385B-108
6	48	100.0	97	4	US-09-280-028-4
7	48	100.0	100	2	US-08-308-494A-19
8	48	100.0	105	3	US-08-434-000A-12
9	48	100.0	105	4	US-09-312-157-12
10	48	100.0	110	3	US-08-836-561-33
11	48	100.0	129	2	US-08-116-778E-2
12	48	100.0	129	2	US-08-438-562-2
13	48	100.0	129	2	US-08-483-528B-92
14	48	100.0	130	4	US-09-393-385B-111
15	48	100.0	130	4	US-09-393-385B-113
16	48	100.0	133	2	US-08-116-778E-37
17	48	100.0	133	2	US-08-438-562-37
18	48	100.0	133	2	US-08-483-528B-101
19	48	100.0	222	2	US-08-190-199A-67
20	48	100.0	235	2	US-08-190-199A-61
21	48	100.0	270	2	US-08-652-507-2
22	48	100.0	553	2	US-08-661-052-16
23	48	100.0	553	4	US-09-188-082-16
24	48	100.0	553	4	US-09-384-088-16
25	48	100.0	553	4	US-09-102-716-16
26	47	97.9	106	1	US-07-634-278-1
27	47	97.9	106	1	US-07-634-278-7

28	47	97.9	106	1	US-07-634-278-8	Sequence 8, Appli
29	47	97.9	106	1	US-07-634-278-16	Sequence 16, Appli
30	47	97.9	106	1	US-08-477-728-1	Sequence 1, Appli
31	47	97.9	106	1	US-08-477-728-7	Sequence 7, Appli
32	47	97.9	106	1	US-08-477-728-8	Sequence 8, Appli
33	47	97.9	106	1	US-08-477-728-16	Sequence 16, Appli
34	47	97.9	106	1	US-08-474-040-1	Sequence 1, Appli
35	47	97.9	106	1	US-08-474-040-7	Sequence 7, Appli
36	47	97.9	106	1	US-08-474-040-8	Sequence 8, Appli
37	47	97.9	106	1	US-08-474-040-16	Sequence 16, Appli
38	47	97.9	106	1	US-08-487-200-1	Sequence 1, Appli
39	47	97.9	106	1	US-08-487-200-7	Sequence 7, Appli
40	47	97.9	106	1	US-08-487-200-8	Sequence 8, Appli
41	47	97.9	106	1	US-08-487-200-16	Sequence 16, Appli
42	47	97.9	106	1	US-08-488-113B-163	Sequence 163, App
43	47	97.9	106	1	US-08-488-113B-165	Sequence 165, App
44	47	97.9	106	1	US-08-477-484B-163	Sequence 163, App
45	47	97.9	106	1	US-08-477-484B-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-08-116-778E-9
Sequence 9, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-778E-9
Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 SASSSVSYMH 10
|||||

Db 1 SASSSVSYMH 10

RESULT 2

US-08-438-562-9
; Sequence 9, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIOHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-438-562-9

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 1 SASSSVSYMH 10

RESULT 3

US-08-483-528B-97
; Sequence 97, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIOHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,528B

FILING DATE: 07-JUN-95

CLASSIFICATION: 536

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-483-528B-97

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10

Db 1 SASSSVSYMH 10

RESULT 4

US-08-836-561-49
; Sequence 49, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:

APPLICANT: KOIKE, Masamichi

APPLICANT: FURUYA, Akiko

APPLICANT: NAKAMURA, Kazuyasu

APPLICANT: IIDA, Akihiro

APPLICANT: ANAZAWA, Hideharu

APPLICANT: HANAI, No. 6018032uo

APPLICANT: TAKATSU, Kiyoshi

TITLE OF INVENTION: Antibody Against Human Interleukin-5

TITLE OF INVENTION: Receptor Alpha Chain

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,561

FILING DATE: 09-MAY-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 232384/95

FILING DATE: 11-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Lawrence, III, Stanton T

REGISTRATION NUMBER: 25,736

REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-561-49

Query Match 100.0%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
|||||
Db 1 SASSSVSVMH 10

RESULT 5

US-09-393-385B-108
Sequence 108, Application US/09393385B
Patent No. 6423511

GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, HAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-393-385B-108

Query Match 100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
|||||
Db 1 SASSSVSVMH 10

RESULT 6

US-09-280-028-4
Sequence 4, Application US/09280028
Patent No. 6241961

GENERAL INFORMATION:

APPLICANT: BENES, IVAN FRIEDRICH
APPLICANT: BOSSLET, KLAUS
TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
FILE REFERENCE: BENES
CURRENT APPLICATION NUMBER: US/09/280,028
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 199 11 329.7
EARLIER FILING DATE: 1999-03-15
EARLIER APPLICATION NUMBER: 198 13 687.0
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 97
TYPE: PRT
ORGANISM: Mus musculus
US-09-280-028-4

Query Match 100.0%; Score 48; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSVMH 10
|||||
Db 16 SASSSVSVMH 25

RESULT 7

US-08-308-494A-19
Sequence 19, Application US/08308494A
Patent No. 5959083

GENERAL INFORMATION:

APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-519

Query Match 100.0%; Score 48; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db 21 SASSSVSVMH 30

RESULT 8
US-08-434-000A-12
; Sequence 12, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 1
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-434-000A-12

Query Match 100.0%; Score 48; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db 24 SASSSVSVMH 33

RESULT 9
US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303441
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-312-157-12

Query Match 100.0%; Score 48; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10
Db 24 SASSSVSVMH 33

RESULT 10
US-08-836-561-33
; Sequence 33, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu

```
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-561-33

Query Match 100.0%; Score 48; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 27 SASSSVSYMH 36

RESULT 11
US-08-116-778E-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22...-1
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24...33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49...55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88...96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; US-08-116-778E-2

Query Match 100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 46 SASSSVSYMH 55

RESULT 12
US-08-438-562-2
; Sequence 2, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: NIXON & VANDERHVE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22...-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24...33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49...55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88...96
IDENTIFICATION METHOD: BY SIMILARITY
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IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2
Query Match 100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
Db 46 SASSSVSYMH 55

RESULT 13
US-08-483-528B-92
; Sequence 92, Application US/08483528B

Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KIWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22...-1
IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
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FEATURE:
NAME/KEY: domain
LOCATION: 24...33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
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FEATURE:
NAME/KEY: domain
LOCATION: 49...55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88...96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-483-528B-92
Query Match 100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
Db 46 SASSSVSYMH 55

RESULT 14

US-09-393-385B-111
; Sequence 111, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-393-385B-111

Query Match 100.0%; Score 48; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
| | | | | | | | | |
Db 46 SASSSVSYMH 55

RESULT 15

US-09-393-385B-113
; Sequence 113, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-393-385B-113

Query Match 100.0%; Score 48; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASSSVSYMH 10
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Db 46 SASSSVSYMH 55

Search completed: December 23, 2002, 07:33:14
Job time : 2.80233 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:20:23 ; Search time 1.26163 Seconds
(without alignments)
163.250 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	31	100.0	7	US-08-438-562-10	Sequence 10, Appl
3	31	100.0	7	US-08-483-528B-98	Sequence 98, Appl
4	31	100.0	7	US-09-171-945-27	Sequence 27, Appl
5	31	100.0	7	US-09-393-385B-109	Sequence 109, App
6	31	100.0	100	US-08-308-494A-15	Sequence 15, Appl
7	31	100.0	105	US-08-434-000A-12	Sequence 12, Appl
8	31	100.0	105	US-09-312-157-12	Sequence 12, Appl
9	31	100.0	107	US-09-171-945-50	Sequence 50, Appl
10	31	100.0	107	US-09-171-945-61	Sequence 61, Appl
11	31	100.0	107	US-09-171-945-65	Sequence 65, Appl
12	31	100.0	107	US-09-171-945-71	Sequence 71, Appl
13	31	100.0	108	US-08-483-749A-8	Sequence 8, Appl
14	31	100.0	108	US-09-171-945-9	Sequence 9, Appl
15	31	100.0	129	US-08-116-778E-2	Sequence 2, Appl
16	31	100.0	129	US-08-438-562-2	Sequence 2, Appl
17	31	100.0	129	US-08-483-528B-92	Sequence 92, Appl
18	31	100.0	130	US-09-393-385B-111	Sequence 111, App
19	31	100.0	130	US-09-393-385B-113	Sequence 113, App
20	31	100.0	133	US-08-116-778E-37	Sequence 37, Appl
21	31	100.0	133	US-08-438-562-37	Sequence 37, Appl
22	31	100.0	133	US-08-483-528B-101	Sequence 101, App
23	31	100.0	213	US-08-630-820-6	Sequence 6, Appl
24	31	100.0	215	5455030-3	Patent No. 5455030
25	31	100.0	225	5455030-5	Patent No. 5455030
26	31	100.0	235	US-09-171-945-17	Sequence 17, Appl
27	31	100.0	235	US-09-171-945-52	Sequence 52, Appl

28	31	100.0	235	4	US-09-171-945-97	Sequence 97, Appl
29	31	100.0	235	4	US-09-171-945-99	Sequence 99, Appl
30	31	100.0	236	6	5455030-7	Patent No. 5455030
31	31	100.0	244	1	US-08-230-843-2	Sequence 2, Appl
32	31	100.0	244	2	US-08-636-936-2	Sequence 2, Appl
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34	31	100.0	248	6	5455030-11	Patent No. 5455030
35	31	100.0	270	2	US-08-652-507-2	Sequence 2, Appl
36	31	100.0	281	4	US-09-423-439-44	Sequence 44, Appl
37	31	100.0	553	2	US-08-661-052-16	Sequence 16, Appl
38	31	100.0	553	4	US-09-188-082-16	Sequence 16, Appl
39	31	100.0	553	4	US-09-364-088-16	Sequence 16, Appl
40	31	100.0	553	4	US-09-102-716-16	Sequence 16, Appl
41	31	100.0	666	4	US-09-423-439-51	Sequence 51, Appl
42	28	90.3	7	3	US-08-783-853A-13	Sequence 13, Appl
43	28	90.3	7	4	US-09-280-028-14	Sequence 14, Appl
44	28	90.3	7	4	US-09-344-050-13	Sequence 13, Appl
45	28	90.3	20	1	US-07-678-974D-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-116-778E-10
; Sequence 10, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-778E-10

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
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Db 1 STSNLAS 7

RESULT 2

US-08-438-562-10
; Sequence 10, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-95

APPLICATION NUMBER: US/08/438,562
CLASSIFICATION: 424

PRIORITY INFORMATION:

APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93

CLASSIFICATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO:

10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-438-562-10

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 3

US-08-483-528B-98
; Sequence 98, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B

FILING DATE:

07-JUN-95

CLASSIFICATION:

536

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO:

98:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-483-528B-98

Query Match

100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 4

US-09-171-945-27
; Sequence 27, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:

APPLICANT: Emery, Stephen

APPLICANT: Copley, Clive Graham

APPLICANT: Edge, Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

Antibody and their Therapeutic Use in an Adept System

FILE REFERENCE: Monoclonal Antibody to CEA

CURRENT APPLICATION NUMBER: US/09/171,945

CURRENT FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: GB9703103.3

PRIOR FILING DATE: 1997-02-14

PRIOR APPLICATION NUMBER: GB9609405.7

PRIOR FILING DATE: 1996-05-04

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29

NUMBER OF SEQ ID NOS: 131

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 27

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-27

Query Match

100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 5
US-09-393-385B-109
; Sequence 109, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KOWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-393-385B-109

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 1 STSNLAS 7

RESULT 6
US-08-308-494A-15
; Sequence 15, Application US/08308494A
; Patent No. 5959083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetravalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-308-494A-15

Query Match 100.0%; Score 31; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 46 STSNLAS 52

RESULT 7
US-08-434-000A-12
; Sequence 12, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-3510

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

TOPOLOGY: DESCRIPTION: Guy's 13 Kappa

US-08-434-000A-12

Query Match 100.0%; Score 31; DB 3; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 8

US-09-312-157-12

Sequence 12; Application US/09312157

Patent No. 6303341

GENERAL INFORMATION:

APPLICANT: ANDREW C. HIATT, JULIAN

K.-C. MA, THOMAS LEHNER

TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon 5 Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/312,157

FILING DATE: 14-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/434,000

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-351

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: Guy's 13 Kappa

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-312-157-12

Query Match 100.0%; Score 31; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 9

US-09-171-945-50

Sequence 50; Application US/09171945

Patent No. 6277599

GENERAL INFORMATION:

APPLICANT: Emery, Stephen

APPLICANT: Copley, Clive Graham

APPLICANT: Edge, Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

Antibody, and Their Therapeutic Use in an Adept System

FILE REFERENCE: Monoclonal Antibody to CEA

CURRENT APPLICATION NUMBER: US/09/171,945

CURRENT FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: GB9703103.3

PRIOR FILING DATE: 1997-02-14

PRIOR APPLICATION NUMBER: GB9609405.7

PRIOR FILING DATE: 1996-05-04

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29

NUMBER OF SEQ ID NOS: 131

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 50

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-50

Query Match

Best Local Similarity 100.0%; Score 31; DB 4; Length 107;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 10

US-09-171-945-61

Sequence 61; Application US/09171945

Patent No. 6277599

GENERAL INFORMATION:

APPLICANT: Emery, Stephen

APPLICANT: Copley, Clive Graham

APPLICANT: Edge, Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

Antibody, and Their Therapeutic Use in an Adept System

FILE REFERENCE: Monoclonal Antibody to CEA

CURRENT APPLICATION NUMBER: US/09/171,945

CURRENT FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: GB9703103.3

PRIOR FILING DATE: 1997-02-14

PRIOR APPLICATION NUMBER: GB9609405.7

PRIOR FILING DATE: 1996-05-04

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29

NUMBER OF SEQ ID NOS: 131

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 61

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-61

Query Match      100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 11
US-09-171-945-65
; Sequence 65, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171.945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 65
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-65

Query Match      100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 12
US-09-171-945-71
; Sequence 71, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171.945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-71

Query Match      100.0%; Score 31; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 13
US-08-483-749A-8
; Sequence 8, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-8

Query Match      100.0%; Score 31; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 51 STSNLAS 57

RESULT 14
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
```

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; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match 100.0%; Score 31; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 15
US-08-116-778E-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NORIO
; APPLICANT: KURANA, YOSHITHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; LOCATION: -22..-1
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; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-116-778E-2
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Query Match 100.0%; Score 31; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 STSNLAS 7
Db 71 STSNLAS 77
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Search completed: December 23, 2002, 07:33:14
Job time : 1.26163 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:08 ; Search time 3.75775 Seconds
(without alignments)
248.221 Million cell updates/sec

Title: US-09-865-198-5

Perfect score: 31

Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	31	100.0	7	AAW41383	CDR2 of light chain
2	31	100.0	7	AAW73170	CDR2 of light chain
3	31	100.0	7	AAW28391	Peptide fragment f
4	31	100.0	7	AAW97233	Complementary dete
5	31	100.0	7	AAW10005	H. pylori 26 kDa p
6	31	100.0	7	AAE13141	Humanised antibody
7	31	100.0	7	AAW82707	VEGF antagonist an
8	31	100.0	7	AAW81968	Ganglioside GD2 sp
9	31	100.0	7	AAW83164	Mouse ganglioside
10	31	100.0	7	AAW63992	Complementarity de

11	31	100.0	7	23	AAU81254	Murine trkC antibo
12	31	100.0	7	23	AAU74410	Light chain comple
13	31	100.0	8	23	AAW80315	Anti-human TNF- α p
14	31	100.0	92	20	AAW89175	Anti-p53 monoclon
15	31	100.0	93	23	ABP02151	Human ORFX protein
16	31	100.0	100	11	AAW07319	VK domain of antib
17	31	100.0	100	17	AAW14487	Monoclonal antibod
18	31	100.0	100	17	AAW99876	Monoclonal antibod
19	31	100.0	102	22	AAW62264	Light chain constr
20	31	100.0	105	17	AAW03182	Guy's 13 anti-Stre
21	31	100.0	106	22	AAE13144	Humanised antibody
22	31	100.0	106	23	AAW74418	Antigen-binding pr
23	31	100.0	107	18	AAW41397	Anti-CEA antibody
24	31	100.0	107	18	AAW41400	Humanised antibody
25	31	100.0	107	18	AAW41401	Humanised antibody
26	31	100.0	107	18	AAW41390	Anti-CEA antibody
27	31	100.0	107	22	AAW83159	Mouse ganglioside
28	31	100.0	107	22	AAW83167	Ganglioside GM2 an
29	31	100.0	107	22	AAW63987	Amino acid sequenc
30	31	100.0	108	13	AAW21294	Murine VL kappa gr
31	31	100.0	108	13	AAW21290	Murine VL kappa gr
32	31	100.0	108	16	AAW79884	Anti-EGFR antibody
33	31	100.0	108	18	AAW41388	Anti-CEA antibody
34	31	100.0	108	21	AAW97236	Variable light cha
35	31	100.0	108	21	AAW10021	H. pylori 26 kDa p
36	31	100.0	108	21	AAW90815	33F8 hybridoma VL
37	31	100.0	108	21	AAW53591	Light chain from a
38	31	100.0	108	21	AAW59306	DC8 light chain va
39	31	100.0	108	22	AAW82710	VEGF antagonist an
40	31	100.0	108	23	AAW74413	Antigen-binding pr
41	31	100.0	108	23	AAW80318	Anti-human TNF- α p
42	31	100.0	109	22	AAW81971	Ganglioside GD2 sp
43	31	100.0	109	22	AAW81974	Ganglioside GD2 sp
44	31	100.0	109	23	AAW81278	Murine trkC antibo
45	31	100.0	110	13	AAW21287	Murine VL kappa gr

ALIGNMENTS

RESULT 1
AAW41383
ID AAW41383 standard; peptide; 7 AA.
AC AAW41383;
XX
DT 02-JUN-1998 (first entry)
XX
DE CDR2 of light chain of anti-CEA antibody.
XX
KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
XX cancer diagnosis; complementarity determining region; light chain.
OS Synthetic.
XX
PN WO9742329-A1.
XX
PD 13-NOV-1997.
XX
PF 29-APR-1997; 97WO-GB01165.
XX
PR 14-FEB-1997; 97GB-0003103.
PR 04-MAY-1996; 96GB-0009405.
XX
PA (ZENE) ZENECA LTD.
XX
PI Copley CG, Edge MD, Emery SC;
XX
DR WPI; 1997-558987/51.
XX
PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
XX diagnosis and therapy of cancer

PS Claim 1; Page 196; 208pp; English.

XX This sequence represents a complementarity determining region (CDR) of
CC the light chain of the antibody of the invention. The antibody is an
CC anti-CEA (carcinoembryonic antigen) antibody (806.077 AB). Host cells or
CC transgenic organisms transformed with DNA encoding the antibody, are used
CC to make the antibody or conjugate. The conjugate is used in a medicament
CC suitable for intravenous administration. The conjugate can be used for
CC cancer therapy, selectively killing tumour cells. The antibody can be
CC used for *in vivo* or *in vitro* diagnosis of cancer.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 2

AAW73170

ID AAW73170 Standard; peptide; 7 AA.

XX AC

XX AC

XX DT

XX DE 22-JAN-1999 (first entry)

XX DE

XX KW CDR2 of light chain of ganglioside GM2 targeting antibody.

XX KW

XX KW Ganglioside GM2; antibody; complementarity determining region; cancer;

XX KW anti-tumour agent.

XX OS Homo sapiens.

XX PN JPL0257833-A.

XX PD 29-SEP-1998.

XX PF 19-MAR-1997; 97JP-0066981.

XX PR 19-MAR-1997; 97JP-0066981.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX XX WPI; 1998-575904/49.

XX DR

XX PT A human type complementarity determining region transplanted

XX PT antibody against ganglioside GM2 - useful as an anti-tumour agent

XX PT and as a diagnostic for related cancers

XX PS Claim 1; Page 29; 66pp; Japanese.

XX XX

XX CC This sequence represents a complementarity determining region (CDR) from

XX CC the heavy chain of the antibody of the invention. The antibody of the

XX CC invention is a human CDR transplanted antibody that reacts specifically

XX CC with ganglioside GM2. DNA encoding the antibody, and vectors and

XX CC transformants containing it, can be used for the recombinant production

XX CC of the antibody. The antibody itself can be used as an anti-tumour agent

XX CC or as a diagnostic tool for related cancers. The antibody has antitumour

XX CC activity against ganglioside GM2 positive cells.

XX XX

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 3

AAV28391

ID AAV28391 standard; Protein; 7 AA.

XX AC

XX AC AAV28391;

XX DT 04-NOV-1999 (first entry)

XX DE

XX DE Peptide fragment from the human anti-GM2 light chain in REI.

XX XX

XX KW antibody; REI; complementarity determining region; CDR;

XX KW chimeric; light chain; heavy chain.

XX OS Homo sapiens.

XX PN US5939532-A.

XX PD 17-AUG-1999.

XX PF 07-JUN-1995; 95US-0483528.

XX PR 07-JUN-1995; 95US-0483528.

XX PR 07-SEP-1993; 93US-0116778.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX XX Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;

XX PI Shitara K;

XX DR WPI; 1999-468416/39.

XX XX

XX PT Chimeric human antibody expression vectors

XX PS

XX PS Example 2; Column 157; 188pp; English.

XX CC The sequences AAV28390 to AAV28392 replace the CDR regions of the NEWM

XX CC DNA and they produce AAV28394, the HKM796L human anti-GM2 antibody light

XX CC chain.

XX CC Chimeric human antibodies of the invention are useful in the treatment

XX CC of cancer, especially that which is of neural ectodermal origin.

XX CC In contrast to prior art constructs based on mouse monoclonal

XX CC antibodies, the chimeric human antibodies do not cause anti-mouse

XX CC immunoglobulin production.

XX CC The chimeric human antibodies have a prolonged half-life and a reduced

XX CC frequency of adverse effects when compared to mouse monoclonal

XX CC antibodies.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 4

AAV97233

ID AAV97233 standard; Protein; 7 AA.

XX AC

XX AC AAV97233;

XX DT 19-DEC-2000 (first entry)

XX DE

XX DE Complementarity determining region (CDRL2) of anti-SI(KDR) antibody.

XX KW Immunoglobulin; antibody; complementary determining region; CDR;

XX KW VEGF; vascular endothelial growth factor; KDR;

XX KW kinase insert domain containing receptor; multivalent; monovalent;

KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW glioblastoma multiforme; hemangioblastoma; AIDS;
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW acquired immune deficiency syndrome; AIDS; human.
OS Homo sapiens.
OS Synthetic.
XX WO200044777-A1.
XX PD 03-AUG-2000.
XX PF 28-JAN-2000; 2000WO-US02180.
XX PR 29-JAN-1999; 99US-0117726.
XX PR 29-JAN-1999; 99US-0240736.
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z, Witte L;
XX PI WPI: 2000-505966/45.
XX DR N-PSDB; AAA53765.
XX PT Novel immunoglobulin molecules binding kinase insert domain-containing
PT receptor with the same affinity as vascular endothelial growth factor,
PT used to reduce tumour growth
XX Claim 3; Page 50; 55pp; English.
XX CC New immunoglobulin molecules are described that bind kinase insert
CC domain-containing receptor (KDR) with a comparable affinity to human
CC vascular endothelial growth factor (VEGF). The antibodies neutralise
CC KDR activation. The immunoglobulin may be a multivalent single
CC chain antibody, a monovalent single chain antibody, a diabody, a
CC triabody, a humanised antibody or a chimerised antibody.
CC The immunoglobulin molecules bind specifically to an
CC extracellular domain of the KDR receptor with the same affinity as
CC VEGF. Overexpression of VEGF has been implicated in a number of
CC human tumour cell lines including glioblastoma multiforme,
CC hemangioblastoma, central nervous system neoplasms and AIDS
CC associated Kaposi's sarcoma. The antibodies therefore have
CC applications in treating these conditions. This sequence encodes a
CC preferred heavy chain complementary determining region of the
CC immunoglobulins of the invention.
SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 1 STSNLAS 7
RESULT 5
AAB10005
ID AAB10005 standard; Protein; 7 AA.
XX AC AAB10005;
XX DT 01-NOV-2000 (first entry)
XX DE H. pylori 26 kDa protein-binding antibody light chain CDR2 peptide.
XX ACid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; light chain; complementarity determining region;
KW CDR.
XX Unidentified.
XX OS

PN WO200026671-A1.
XX PD 11-MAY-2000.
XX PF 29-OCT-1999; 99WO-EP08212.
XX PR 29-OCT-1998; 98EP-0120517.
XX PR 06-NOV-1998; 98EP-0120687.
XX PA (CONN-) CONNEX GMBH.
XX PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
XX PI Ringeis A;
XX DR WPI: 2000-365747/31.
XX DR N-PSDB; AAA40161.
XX PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT pylori, comprises reacting a faecal sample with two binding reagents for
PT antigens that survive intestinal passage
XX Claim 24; Page 21; 84pp; German.
XX CC This invention describes a novel method for the detection of a mammalian
CC infection by an acid-resistant microorganism (A) by treating a faecal
CC sample with at least two different monoclonal antibodies (MAB) (or their
CC fragments or derivatives) or aptamers (collectively (I)) and detecting
CC formation of a complex (C) between (I) and the corresponding antigen of
CC (A). The first and second (I) bind to epitopes of different antigens
CC (Ag). These epitopes are present, after passage through the intestines,
CC in at least some mammals, and have either: (i) their native structure,
CC or (ii) a structure against which an antibody is produced by an animal
CC infected or immunized with (A), or its extract, lysate, derived protein
CC or fragment, or with a synthetic peptide. Practically all mammals display
CC at least one of the specified epitopes. The method is used to detect
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
CC therapeutically. The method is direct and non-invasive, and provides an
CC inexpensive and easily standardizable diagnosis, despite possible
CC degradation of antigens during passage through the intestines. This
CC sequence represents a fragment of a H. pylori 26 kDa protein-binding
CC antibody light chain complementarity determining region CDR2 which is
CC used to illustrate the method of the invention.
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 1 STSNLAS 7
RESULT 6
AAE13141
ID AAE13141 standard; peptide; 7 AA.
XX AC AAE13141;
XX DT 28-JAN-2002 (first entry)
XX DE Humanised antibody murine light chain hypervariable region (VL) CDR2.
XX KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW cytosolic; light chain hypervariable region; VL; myelocytic leukaemia;
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
XX Mus sp.
XX OS

PN WO200174296-A2.
 XX 11-OCT-2001;
 PD 30-MAR-2001; 2001WO-US10504.
 XX 31-MAR-2000; 2000US-0540770.
 PF (IMCL-) IMCLONE SYSTEMS INC.
 XX (CORR) CORNELL RES FOUND INC.
 PA Witte L, Rafii S;
 PI WPI: 2001-662942/76.
 XX N-PSDB; AAD21667.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with
 PT an antagonist of a vascular endothelial growth factor receptor -
 XX Claim 8; Page 15; 68pp; English.

XX The invention relates to a method for inhibiting the growth of non-solid
 CC tumor cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to
 CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
 CC antibody murine light chain hypervariable region (VL) CDR-2 used in the
 CC exemplification of the invention.

XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 31; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STSNLAS 7
 Db 1 STSNLAS 7

RESULT 7
 AAB82707
 ID AAB82707 standard; Peptide; 7 AA.
 XX AAB82707;
 AC
 XX 15-OCT-2001 (first entry)
 DT
 XX VEGF antagonist antibody IMC-1C11 VL CDR-2.

XX IMC-1C11, chimeric antibody; mouse; human; antagonist; VEGF;
 KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
 KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
 KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
 KW colon carcinoma; ovarian carcinoma; neuroblastoma;
 KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
 KW complementarity determining region.

XX Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX WO200154723-A1.
 PN 02-AUG-2001.
 XX

PF 29-JAN-2001; 2001WO-US02839.
 XX 28-JAN-2000; 2000US-0178791.
 PR 31-MAR-2000; 2000US-0539692.
 XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX Kerbel R;
 XX WPI: 2001-514531/56.
 DR Treating or controlling an angiogenic dependent condition (e.g. a
 XX neoplasm, collagen-vascular or autoimmune disease) in mammal by
 PT administering a combination of an antiangiogenic molecule and a
 PT chemotherapeutic agent -
 XX Disclosure; Page 37; 42pp; English.
 PS The present sequence is that of complementarity determining region
 XX 2 of the light chain variable region (see also AAB82702) of
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,
 CC or a fragment of it, can be used as an anti-angiogenic molecule,
 CC together with a chemotherapeutic acid, for the treatment of an
 CC angiogenic dependent condition in a mammal, especially a human.
 CC The invention relates generally to a method of treating or
 CC controlling an angiogenic dependent condition by administering an
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
 CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The anti-angiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STSNLAS 7
 Db 1 STSNLAS 7

RESULT 8
 AAB81968
 ID AAB81968 standard; Peptide; 7 AA.

XX AAB81968;
 AC
 XX 03-JUL-2001 (first entry)
 DT

XX Ganglioside GD2 specific antibody related peptide SEQ ID NO: 7.
 DE Ganglioside; GD2; complementation determining region; CDR; antibody;
 XX mouse; cancer.

XX Mus musculus.
 OS WO200123573-A1.
 PN 05-APR-2001.
 XX

XX 29-SEP-2000; 2000WO-JP06773.
 XX 30-SEP-1999; 99JP-0278290.
 PR

XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Hanai N, Shitara K, Nakamura K, Niwa R;
 PI WPI; 2001-266163/27.
 XX
 DR
 XX Human type complementation-determining domain transplanted antibody and
 PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
 PT e.g. tumours, has low antigenicity, little side effects but potent
 PT activity in cancer -
 XX
 PS Claim 6; Page 100; 123pp; Japanese.
 XX
 CC The present invention describes an antibody, which can react specifically
 CC with ganglioside GD2, and is transplanted with a human type
 CC complementation-determining domain (CDR), or its fragments. The antibody
 CC and its derivatives are useful in diagnosis and therapy of tumours,
 CC particularly cancer diagnosis. The present sequence is a peptide
 CC used in the exemplification of the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 Db | | | | | | |
 1 STSNLAS 7
 RESULT 9
 AAB83164
 ID AAB83164 standard; peptide; 7 AA.
 XX
 AC AAB83164;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Mouse ganglioside GM2 antibody light chain variable region CDR2.
 XX
 KW Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer;
 KW complementarity determining region; CDR.
 XX
 OS Mus sp.
 XX
 PN WO200123431-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP06775.
 XX
 PR 30-SEP-1999; 99JP-0278292.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Hanai N, Nakamura K, Niwa R;
 XX
 WPI; 2001-266142/27.
 XX
 PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
 PT radioisotopes or proteins for treatment and diagnosis of cancer -
 XX
 PS Claim 4; Page 72; 80pp; Japanese.
 XX
 CC The present invention relates to derivatives of an antibody against
 CC ganglioside GM2. The antibody may be a monoclonal antibody or its
 CC fragments. The antibody is combined with a radioactive isotope,
 CC protein or small drug in the treatment and diagnosis of cancer.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 Db | | | | | | |
 1 STSNLAS 7
 RESULT 11
 AAU81254
 ID AAU81254 standard; Peptide; 7 AA.

Query Match 100.0%; Score 31; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 Db | | | | | | |
 1 STSNLAS 7
 RESULT 10
 AAG63992
 ID AAG63992 standard; peptide; 7 AA.
 XX
 AC AAG63992;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Complementarity determining region of light chain of antibody 2C4.
 DE
 KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
 KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
 KW leukemia; eosinophil.
 XX
 OS Mus sp.
 XX
 PN WO200166126-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US07193.
 XX
 PR 07-MAR-2000; 2000US-0187595.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
 PI Schleimer R;
 XX
 WPI; 2001-570749/64.
 XX
 PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for
 PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
 PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal -
 XX
 PS Claim 10; Page 34; 35pp; English.
 XX
 CC AAG63991-93 represent the complementarity determining regions (CDRs)
 CC of the light chain variable region of murine monoclonal antibody 2C4.
 CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The
 CC antibody is useful for treating or preventing allergic rhinitis,
 CC allergies, asthma, anemia, eczema or diseases such as lymphoma,
 CC leukemia or systemic mastocytosis in a mammal. It is also useful for
 CC detecting the presence of a cell, especially eosinophil in a sample,
 CC by detecting binding of the antibody to SAF-2. The antibody can be
 CC coupled to toxins, antiproliferative drugs or radionuclides to
 CC kill cells in areas of excessive SAF-2 expression.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 Db | | | | | | |
 1 STSNLAS 7
 RESULT 11
 AAU81254
 ID AAU81254 standard; Peptide; 7 AA.

XX AC AAU81254;
 XX DT 09-APR-2002 (first entry)
 XX DE Murine trkC antibody light chain CDR2 of variable region #2.
 XX KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
 KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
 KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
 KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
 KW nerve cell injury; blood cell disorder; leukopenia; eosinopenia; wound;
 KW basopenia; lymphopenia; monocytopenia; neutropenia; cancer; ulcer;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
 KW cellular degeneration; gene therapy.
 XX OS Mus sp.
 XX PN WO200198361-A2.
 XX PD 27-DEC-2001.
 XX PF 22-JUN-2001; 2001WO-US20153.
 XX PR 22-JUN-2000; 2000US-213141P.
 XX PR 05-OCT-2000; 2000US-238319P.
 XX PA (GETH) GENENTECH INC.
 XX PI Devaux B; Hongo JS, Presta LG, Shelton DL;
 XX DR WPI; 2002-130790/17.
 XX PT Novel anti-trkC agonist monoclonal antibody useful for treating
 PT neurodegenerative disease, shows no significant cross-reactivity with
 PT trkA/trkB, and recognizes epitope in domain 5 of trkC
 XX PS Claim 13; Fig 11; 121pp; English.
 XX CC The invention relates to an anti-trkC agonist monoclonal antibody which
 CC shows no significant cross-reactivity with trkA or trkB, and recognizes
 CC an epitope in domain 5 of trkC. The antibodies of the invention are
 CC effective in the treatment of cisplatin- or pyridoxine-induced
 CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
 CC sensory neuropathy, neurodegenerative disease including amyotrophic
 CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
 CC cells such as leukopenia including eosinopenia, basopenia,
 CC lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and tumours. The sequences are
 CC also useful for inducing angiogenesis for treating wounds, ulcers and
 CC diabetic complications of sickle cell disease, for treating cardiac
 CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
 CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
 CC human and mouse anti-trkC agonist monoclonal antibodies and antibody
 CC fragments of the invention.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 Db 1 STSNLAS 7
 RESULT 12
 AAU74410
 ID AAU74410 standard; peptide; 7 AA.
 XX AC AAU74410;

XX DT 26-MAR-2002 (first entry)
 XX DE Light chain complementarity determining region L2 (CDRL2).
 XX KW Complementarity determining region; CDR; CDRL2; antigen; cytostatic;
 KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
 KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
 KW antibody light chain variable domain.
 XX OS Mus sp.
 XX PN WO200190192-A2.
 XX PD 29-NOV-2001.
 XX PF 24-MAY-2001; 2001WO-US16924.
 XX PR 24-MAY-2000; 2000US-206749P.
 XX PA (IMCL-) IMCLONE SYSTEMS INC.
 XX PI Zhu Z;
 XX DR WPI; 2002-106189/14.
 XX DR N-PSDB; AAS20281.
 XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumour growth and for inhibiting angiogenesis, comprises a complex of
 PT two polypeptides and two second polypeptides
 XX PS Claim 55; Page 57; 64pp; English.
 XX CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This peptide sequence represents the light chain variable domain
 CC complementarity determining region L2 (CDRL2) incorporated into an
 CC antigen-binding protein described in the method of the invention.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 Db 1 STSNLAS 7
 RESULT 13
 AAG80315
 ID AAG80315 standard; peptide; 8 AA.
 XX AC AAG80315;
 XX AC AAG80315;

DT 18-FEB-2002 (first entry)
 XX Anti-human TNF-alpha CDR-L2 peptide.
 XX
 XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
 KW heavy chain; light chain; complementarity determining region; vasotropic;
 KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
 KW rheumatoid arthritis; malaria; multiple sclerosis.
 XX
 XX Homo sapiens.
 XX
 XX WO200179298-A1.
 XX
 XX 25-OCT-2001.
 XX
 XX 18-APR-2001; 2001WO-JP03308.
 XX
 XX 19-APR-2000; 2000JP-0117394.
 XX
 XX (SUNR) SUNTORY LTD.
 XX
 XX Fukuda Y, Nagahira K, Nakanishi T;
 XX
 XX WPI; 2002-066345/09.
 XX
 XX Novel heavy and light-chain polypeptides of chimeric and humanised
 PT antibodies against human tumour necrosis factor alpha for
 PT low-immunogenicity treatment of TNF-related diseases such as toxic
 PT shock syndrome -
 XX
 XX Claim 3b; Page 26; 36pp; Japanese.
 XX
 XX This invention describes novel heavy chain and light chain polypeptides
 CC or their fragments of a recombinant antibody to human TNF-alpha which
 CC contain complementarity determining region (CDR) sequences. The products
 CC of the invention have vasotropic, antiarthritic, neuroprotective and
 CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
 CC vivo. The antibodies are used for producing chimeric and humanised
 CC antibodies that may be used for the treatment and prevention of TNF-alpha
 CC associated diseases such as toxic shock syndrome, rheumatoid arthritis, in
 CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
 CC humans. This sequence represents the anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) light chain CDR1 designated CDR-L2.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 31; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 DB 2 STSNLAS 8
 |||||
 RESULT 14
 AAW89175
 ID AAW89175 standard; peptide; 92 AA.
 XX
 XX AAW89175;
 XX
 XX 25-MAR-1999 (first entry)
 XX
 XX Anti-p53 monoclonal antibody 246 variable light chain sequence.
 DE
 XX Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
 KW immune response; tumour associated antigen; metastatic cancer.
 KW
 XX Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 53

FT Misc-difference 86 /note= "unspecified"
 FT /note= "unspecified"
 FT Misc-difference 90 /note= "unspecified"
 XX
 XX WO9856416-A1.
 PN
 XX 17-DEC-1998.
 PD
 XX
 XX 09-JUN-1998; 98WO-IL00266.
 PF
 XX 09-JUN-1997; 97IL-0121041.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
 PI Wolkowicz R;
 PI
 XX WPI; 1999-070296/06.
 DR
 XX
 XX Use of a monoclonal antibody to a tumour-associated antigen - to
 PT induce anti-tumour immunity or elicit an increased immune response
 PT to the antigen
 PT
 XX
 XX Example 3; Fig 3; 47pp; English.
 PS
 XX The present invention describes the use of an immunogen (A) to induce
 CC anti-tumour immunity; to elicit an increased immune response to tumour
 CC associated antigen (TAA) and/or to induce an immune response to mutant
 CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
 CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR
 CC (complementarity determining region) on the heavy or light chain of Mab
 CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
 CC variable (V) region of Mab, in a gene delivery vehicle. The present
 CC sequence represents the variable light chain sequence from anti-p53 Mab
 CC 246. Also described is a method for generating sequence-specific,
 CC anti-DNA antibodies (Ab) by immunising a mammal with a Mab directed to a
 CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
 CC used to treat a wide variety of primary and metastatic cancers,
 CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
 CC to determine critical sequences in animal or plant breeding); to
 CC identify bacteria and other parasites; to determine parentage; in
 CC forensic science; to isolate specific genes for DNA vaccination; in gene
 CC sequencing and cloning; also possibly for activation of selected
 CC therapeutic genes in plants, animals and humans. (A) induce an effective
 CC anti-tumour response without causing harm to the patient. The method
 CC uses (A) to generate anti-TAA by exploiting the anti-idiotype network.
 XX
 XX Sequence 92 AA;
 SQ
 Query Match 100.0%; Score 31; DB 20; Length 92;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STSNLAS 7
 DB 32 STSNLAS 38
 |||||
 RESULT 15
 ABP02151
 ID ABP02151 standard; Protein; 93 AA.
 XX
 XX AC ABP02151;
 XX
 XX 24-JUN-2002 (first entry)
 DT
 XX Human ORFX protein sequence SEQ ID NO:4284.
 DE
 XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;

KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

OS Homo sapiens.

XX WO200192523-A2.

PN 06-DEC-2001.

PD 29-MAY-2001; 2001WO-US10836.

XX 30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR N-PSDB; ABN17903.

XX Novel human polypeptides and polynucleotides useful for diagnosing,

XX preventing and treating cardiovascular disease, neurodegenerative,

XX hyperproliferative disorders and autoimmune disorders

XX Disclosure; SEQ ID 4284; 1037pp; English.

XX The present invention describes substantially purified human proteins

XX (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

XX in the specification). ABN15762 to ABN27252 encode the human ORFX

XX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for

XX treating or preventing a pathology associated with an ORFX-associated

XX disorder in humans, and in the manufacture of a medicament for treating a

XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide

XX sequences can be used in gene therapy. ORFX sequences can be used in the

XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,

XX psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,

XX osteoarthritis, neurodegenerative disorders, disorders related to organ

XX transplantation, cardiovascular diseases, diabetes mellitus, systemic

XX lupus erythematosus, hypertension, hypothyroidism, cholesterol ester

XX storage disease, various immune deficiencies and disorders, infectious

XX diseases, autoimmune disorders such as multiple sclerosis, rheumatoid

XX arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host

XX disease, and autoimmune inflammatory eye disease. ORFX proteins are also

XX useful for treating burns, incisions, ulcers, for treating osteoporosis,

XX bone degenerative disorders, or periodontal disease, and for gut

XX protection or regeneration and treatment of lung or liver fibrosis,

XX reperfusion injury in various tissues and conditions resulting from

XX systemic cytokine damage.

XX N.B. The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 93 AA;

Query Match 100.0%; Score 31; DB 23; Length 93;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7

DB 15 STSNLAS 21

Search completed: December 23, 2002, 07:25:06

Job time : 4:75775 secs

QY 1 STSNLAS 7
| | | | |
Db 41 STSNLAS 47

RESULT 3

SI17623
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17623
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17623
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 43 STSNLAS 49

RESULT 4

SI17640
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17640
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17640
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 43 STSNLAS 49

RESULT 5

SI17641
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17641
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17641
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 43 STSNLAS 49

RESULT 6

SI17642
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17642
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230; MUID:91326098; PMID:1907718
A:Accession: SI17642
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 43 STSNLAS 49

RESULT 7

SI17643
Ig kappa chain V region (4.68) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C:Accession: C33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: C33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
A:Cross-references: GB:M25999; NID:g197117; PIDN:AAA38915.1; PID:g197118
A:Note: the authors translated the codon TTG for residue 34 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 51 STSNLAS 57

RESULT 8

D38601
Ig kappa chain V region (6A7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: D38601
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: D38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <GOS>
A:Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||

Db 41 STSNLAS 47

RESULT 9

PH1058
Ig light chain V region (clone 163.72) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1058
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1058
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||

Db 51 STSNLAS 57

RESULT 10

PH1059
Ig light chain V region (clone 17s-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1059
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1059
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 51 STSNLAS 57
|||||||

RESULT 11

PH1060
Ig light chain V region (clone 74-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1060
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1060
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||

Db 51 STSNLAS 57

RESULT 12

PT0404
Ig light chain V region (S107/VH11 group 3-23) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: PT0404
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib
A:Reference number: PT0376; MUID:91147903; PMID:1900082
A:Accession: PT0404
A:Molecule type: DNA
A:Residues: 1-109 <BEH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||

Db 51 STSNLAS 57

RESULT 13

PT0405
Ig light chain V region (S107/VH11 group 3-38) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: PT0405
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib
A:Reference number: PT0376; MUID:91147903; PMID:1900082
A:Accession: PT0405
A:Molecule type: DNA
A:Residues: 1-109 <BEH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Job time : 2.38372 secs

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. NO. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 51 STSNLAS 57

RESULT 14

A32513
Ig kappa chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: A32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: A32513
A:Molecule type: DNA
A:Residues: 1-130 <KOF>
A:Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 73 STSNLAS 79

RESULT 15

PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0013
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0013
A:Molecule type: mRNA
A:Residues: 1-140 <CHE>
A:Experimental source: cell line 4C11
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:46-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-118/Region: complementarity-determining 3
F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 100.0%; Score 31; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. NO. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 71 STSNLAS 77

Search completed: December 23, 2002, 07:31:36

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08 : Search time 0.651163 Seconds
(without alignments)
180.208 Million cell updates/sec

Title: US-09-865-198-5
Perfect score: 31
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues
Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	10	US-09-976-787-5
2	31	100.0	7	10	US-09-865-198-5
3	31	100.0	7	10	US-09-910-059-27
4	31	100.0	105	9	US-09-982-107-12
5	31	100.0	106	10	US-09-976-787-24
6	31	100.0	106	10	US-09-865-198-23
7	31	100.0	107	9	US-09-144-886-76
8	31	100.0	107	9	US-09-144-886-88
9	31	100.0	107	10	US-09-910-059-61
10	31	100.0	107	10	US-09-910-059-61
11	31	100.0	107	10	US-09-910-059-65
12	31	100.0	107	10	US-09-910-059-71
13	31	100.0	108	10	US-09-976-787-8
14	31	100.0	108	10	US-09-865-198-8
15	31	100.0	108	10	US-09-910-059-9
16	31	100.0	112	9	US-09-144-886-89
17	31	100.0	235	10	US-09-910-059-17
18	31	100.0	235	10	US-09-910-059-52
19	31	100.0	235	10	US-09-910-059-97

20	31	100.0	235	10	US-09-910-059-99	Sequence 99, Appl
21	31	100.0	238	10	US-09-976-787-29	Sequence 29, Appl
22	31	100.0	238	10	US-09-865-198-28	Sequence 28, Appl
23	31	100.0	240	10	US-09-976-787-28	Sequence 28, Appl
24	31	100.0	240	10	US-09-865-198-27	Sequence 27, Appl
25	31	100.0	669	9	US-09-807-721-2	Sequence 2, Appl
26	28	90.3	7	10	US-09-965-099-13	Sequence 13, Appl
27	28	90.3	7	12	US-10-051-852-13	Sequence 13, Appl
28	28	90.3	8	10	US-09-189-048-16	Sequence 16, Appl
29	28	90.3	8	10	US-09-189-048-28	Sequence 28, Appl
30	28	90.3	27	10	US-09-965-099-55	Sequence 55, Appl
31	28	90.3	27	12	US-10-051-852-55	Sequence 35, Appl
32	28	90.3	93	10	US-09-965-099-35	Sequence 35, Appl
33	28	90.3	93	10	US-09-965-099-66	Sequence 66, Appl
34	28	90.3	93	12	US-10-051-852-35	Sequence 35, Appl
35	28	90.3	93	12	US-10-051-852-66	Sequence 66, Appl
36	28	90.3	106	10	US-09-893-615-89	Sequence 89, Appl
37	28	90.3	106	10	US-09-965-099-105	Sequence 105, App
38	28	90.3	106	12	US-10-051-852-105	Sequence 105, App
39	28	90.3	107	10	US-09-965-099-11	Sequence 11, Appl
40	28	90.3	107	10	US-09-965-099-44	Sequence 44, Appl
41	28	90.3	107	10	US-09-965-099-57	Sequence 57, Appl
42	28	90.3	107	10	US-09-965-099-62	Sequence 62, Appl
43	28	90.3	107	10	US-09-965-099-74	Sequence 74, Appl
44	28	90.3	107	12	US-10-051-852-11	Sequence 11, Appl
45	28	90.3	107	12	US-10-051-852-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-5
; Sequence 5, Application US/09976787
; Patent No. US20020084528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-5

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
| | | | | | |
Db 1 STSNLAS 7

RESULT 2
US-09-865-198-5
; Sequence 5, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-5

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 1 STSNLAS 7

RESULT 3

US-09-910-059-27
; Sequence 27, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Jedge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-27

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 1 STSNLAS 7

RESULT 4

US-09-982-107-12
; Sequence 12, Application US/09982107
; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 12

; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12

Query Match 100.0%; Score 31; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 5

US-09-976-787-24
; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-24

Query Match 100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7
Db 49 STSNLAS 55

RESULT 6

US-09-865-198-23
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23

Query Match 100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||
Db 49 STSNLAS 55

RESULT 7

US-09-144-886-76
; Sequence 76, Application US/09144886
; Patent No. US2002015114A1

; GENERAL INFORMATION:

; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: C9 region VL epitope 1
US-09-144-886-76

Query Match 100.0%; Score 31; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||
Db 49 STSNLAS 55

RESULT 8

US-09-144-886-88
; Sequence 88, Application US/09144886
; Patent No. US2002015114A1

; GENERAL INFORMATION:

; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/a clone
; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88

Query Match 100.0%; Score 31; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||
Db 49 STSNLAS 55

RESULT 9

US-09-910-059-50
; Sequence 50, Application US/09910059
; Patent No. US20020142359A1

; GENERAL INFORMATION:

; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody
; FILE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain variable region
US-09-910-059-50

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||
Db 49 STSNLAS 55

RESULT 10

US-09-910-059-61
; Sequence 61, Application US/09910059
; Patent No. US20020142359A1

; GENERAL INFORMATION:

; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody
; FILE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-61

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
|||||||

Db 49 STSNLAS 55

RESULT 11

US-09-910-059-65
; Sequence 55, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-65

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 12

US-09-910-059-71
; Sequence 71, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-71

Query Match 100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 13

US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
; OTHER INFORMATION: humanised light chain variable region variant
US-09-976-787-8

Query Match 100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 14

US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
; OTHER INFORMATION: humanised light chain variable region variant
US-09-865-198-8

Query Match 100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7

Db 49 STSNLAS 55

RESULT 15

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US-09-910-059-9
; Sequence 9, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-9

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Query Match      100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 STSNLAS 7
   |||||
Db 49 STSNLAS 55

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Job time : 1.65116 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57 ; Search time 1.77907 seconds
(without alignments)
486.327 Million cell updates/sec

Title: US-09-865-198-6
Perfect score: 48
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	132	2 S05268	Ig kappa chain pre
2	42	87.5	93	2 S17641	Ig kappa chain v r
3	42	87.5	106	2 B54378	Ig light chain v r
4	42	87.5	106	2 PS0070	Ig kappa chain v r
5	40	83.3	35	2 E38601	Ig kappa chain v r
6	40	83.3	99	2 D38601	Ig kappa chain v r
7	38	79.2	91	2 S17626	Ig kappa chain v r
8	38	79.2	117	2 S42466	Ig kappa chain v r
9	38	79.2	140	2 PL0013	Ig kappa chain pre
10	37	77.1	106	2 D27887	Ig kappa chain v r
11	37	77.1	130	2 A32513	Ig kappa chain pre
12	37	77.1	132	2 S40334	Ig kappa chain - h
13	37	77.1	1501	1 B29813	174K ninaC protein
14	36	75.0	86	2 C28195	Ig kappa chain v r
15	36	75.0	886	2 F83862	penicillin-binding
16	35	72.9	91	2 S17628	Ig kappa chain v r
17	35	72.9	107	2 A28195	Ig kappa chain v r
18	35	72.9	108	1 KLHUBN	Ig kappa chain v-I
19	35	72.9	108	2 PL0204	anti-DNA autoantib
20	35	72.9	111	2 S23628	Ig kappa chain v r
21	35	72.9	129	2 S40369	Ig kappa chain - h
22	35	72.9	133	2 S49632	hypothetical prote
23	34	70.8	98	2 S26342	Ig kappa chain v r
24	34	70.8	102	2 S29584	Ig kappa chain v r
25	34	70.8	106	2 PC4282	Ig kappa chain (an
26	34	70.8	108	1 K2BGGM	Ig kappa chain v r
27	34	70.8	108	2 S29581	Ig kappa chain v r
28	34	70.8	128	2 S40379	Ig kappa chain v-J
29	34	70.8	129	2 D32513	Ig kappa chain pre

30 34 70.8 144 2 PL0106 Ig kappa chain pre
31 34 70.8 275 2 H82106 chemotaxis protein
32 34 70.8 341 1 VHBPEL major capsid prote
33 34 70.8 341 2 C90833 major capsid prote
34 34 70.8 341 2 F90900 probable major cap
35 34 70.8 341 2 E85690 cysteine proteinas
36 34 70.8 343 1 KHDO cysteine proteinas
37 34 70.8 377 2 T12042 conserved hypoteth
38 34 70.8 380 2 S55923 ABC transporter BH
39 34 70.8 397 2 B70048 probable membrane
40 34 70.8 653 2 S67035 Ig kappa chain v r
41 34 70.8 77 2 D30502 Ig kappa chain v r
42 33 68.8 93 2 S17635 Ig kappa chain v-I
43 33 68.8 108 1 KLHUKU Ig kappa chain v r
44 33 68.8 108 2 PS0069 Ig kappa chain v r
45 33 68.8 108 2 PS0069 Ig kappa chain v r

ALIGNMENTS

RESULT 1

S05268

Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000

C:Accession: S05268; J10062; S03846

R:Levy, S.

submitted to the EMBL Data Library, February 1989

A:Reference number: S05267

A:Accession: S05268

A:Molecule type: mRNA

A:Residues: 1-132 <LEV>

A:Cross-references: EMBL:X14098; NID:g52562; PIDN:CRAA32260.1; PID:g736261

R:Carroll, W.L.; Scarnes, C.O.; Levy, R.; Levy, S.

J. Exp. Med. 168, 1607-1620, 1988

A:Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An expl

A:Reference number: J10061; MUID:89035985; PMID:3141553

A:Accession: J10062

A:Molecule type: mRNA

A:Residues: 1-120 <CAR>

A:Cross-references: EMBL:X14098

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>

F:15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>

F:15-108/Domain: V region (V-kappa-1) <VRE>

F:30-103/Domain: immunoglobulin homology <IMM>

F:109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 100.0%; Score 48; DB 2; Length 132;

Best Local Similarity 100.0%; Pred. No. 0.023; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

Qy 1 QQRSSYPFT 9

Db 102 QQRSSYPFT 110

RESULT 2

S17641

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17641

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17641

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 93;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9

Db 82 QORSSYPPT 90

RESULT 3

Ig light chain V region anti-triplex DNA - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B54378
R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
A:Reference number: B54378; MUID:94165109; PMID:7509814
A:Accession: B54378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <AGA>
A:Cross-references: GB:568985; NID:9545746; PIDN:AAB30096.1; PID:9545747
A:Experimental source: spleen and myeloma cell line MOPC 315.43
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 106;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9

Db 88 QORSSYPPT 96

RESULT 4

PS0070

Ig kappa chain V region (38C13.V6.1) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0070
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0070
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 106;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9

Db 88 QORSSYPPT 96

RESULT 5

E38601

Ig kappa chain V region (14D2) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: E38601
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: E38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-35 <GOS>
A:Cross-references: GB:M57982; NID:g196410; PIDN:AAA63363.1; PID:g196411
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 83.3%; Score 40; DB 2; Length 35;
Best Local Similarity 87.5%; Pred. No. 0.26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QRSSYPPT 9

Db 24 QRSSYPPT 31

RESULT 6

D38601

Ig kappa chain V region (6A7) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: D38601
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: D38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <GOS>
A:Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 40; DB 2; Length 99;
Best Local Similarity 77.8%; Pred. No. 0.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSSYPPT 9

Db 80 QORSSYPPT 88

RESULT 7

S17626

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17626
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17626
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-91 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 91;
Best Local Similarity 88.9%; Pred. No. 1.6;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||||
Db 80 QORSSYPPT 88

RESULT 8
S42466
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42466
R:Shiyonov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42466
A:Accession: S42466
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||||
Db 99 QYSSYPPT 107

RESULT 9
PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0013
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0013
A:Molecule type: mRNA
A:Residues: 1-140 <CHE>
A:Experimental source: cell line 4C11
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:46-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-118/Region: complementarity-determining 3
F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 79.2%; Score 38; DB 2; Length 140;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||||
Db 110 QORSSYPPT 118

RESULT 10
G27887
Ig kappa chain V region (H18-S415) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000

C:Accession: G27887
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: G27887
A:Molecule type: DNA
A:Residues: 1-106 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 106;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QORSSYPPT 9
|||||||
Db 89 QORSSYPPT 96

RESULT 11
A32513
Ig kappa chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: A32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: A32513
A:Molecule type: DNA
A:Residues: 1-130 <KOF>
A:Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 130;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|||||||
Db 112 QYSSYPPT 120

RESULT 12
S40334
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40334
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|| :|||||
Db 110 QQFNSYPPT 118

RESULT 13

B29813
174K ninaC protein - fruit fly (Drosophila melanogaster)
N:Contains: protein kinase (EC 2.7.1.-)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: B29813
R:Montell, C.; Rubinstein, G.M.
Cell 52, 757-772, 1988
A:Title: The Drosophila ninaC locus encodes two photoreceptor cell specific proteins with
A:Reference number: A90898; MUID:88151067; PMID:2449973
A:Accession: B29813
A:Molecule type: mRNA
A:Residues: 1-1501 <MON>
A:Cross-references: GB:M20230; NID:g157967; PIDN:AAA28721.1; PID:g157968
C:Genetics:
A:Gene: FlyBase:ninaC
A:Cross-references: FlyBase:FBgn0002938
C:Superfamily: ninaC protein; myosin motor domain homology; protein kinase homology
C:Keywords: actin binding; alternative splicing; ATP; nucleotide binding; P-loop; phosph
F:14-282/Domain: protein kinase homology <KIN>
F:335-1022/Domain: myosin motor domain homology <MMOT>
F:425-432/Region: nucleotide-binding motif A (P-loop)
F:911-936/Region: actin binding #status predicted
F:1034-1501/Domain: carboxyl-terminal <CBT>
F:45,60,145/Active site: Lys, Glu, Asp #status predicted
F:431/Binding site: ATP (Lys) #status predicted

Query Match 77.1%; Score 37; DB 1; Length 1501;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYP 7
|||:|||||
Db 1352 QORSSYP 1358

RESULT 14

C28195
Ig kappa chain V region (anti-halo-peridol antibody C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-May-1997
C:Accession: C28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Halo-peridol binding to monoclonal antibodies. Hypervariable region amino acid s
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: C28195
A:Molecule type: mRNA
A:Residues: 1-86 <SHE>
A:Cross-references: GB:M19768
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 75.0%; Score 36; DB 2; Length 86;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9
|| :|||||
Db 68 QQXNSYPPT 76

RESULT 15

F83862
penicillin-binding proteins 1A/1B ponA [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: F83862
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-886 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:gl0174030; PIDN:BA05421.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: ponA

Query Match 75.0%; Score 36; DB 2; Length 886;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPPT 8
||:|||||
Db 282 QERESYPPT 289

Search completed: December 23, 2002, 07:31:37
Job time : 2.77907 secs